

Result No.	Score	Query Match	Length	DB	ID	Description	
C 1	601	50.1	649	4	US-09-461-912A-36	Sequence 36, Appl	
C 2	557	46.5	579	4	US-09-461-912A-24	Sequence 24, Appl	
C 3	523	43.6	582	4	US-09-513-998C-14898	Sequence 14898, A	
C 4	485.2	40.5	2016	4	US-10-000-489-1	Sequence 1, Appl	
C 5	329.8	27.5	600	3	US-09-399-913-64	Sequence 64, Appl	
C 6	329.8	27.5	600	4	US-09-350-614-64	Sequence 64, Appl	
C 7	328.4	27.4	570	4	US-09-461-912A-23	Sequence 23, Appl	
C 8	164.8	13.7	276	4	US-09-313-294A-4020	Sequence 4020, Ap	
C 9	164.8	13.7	509	3	US-09-385-982-150	Sequence 150, App	
C 10	101	8.4	131	4	US-09-680-420A-21	Sequence 21, Appl	
C 11	85.8	7.2	522	4	US-09-774-528-41	Sequence 41, App	
C 12	75.2	6.3	592	4	US-09-949-016-5370	Sequence 5370, Ap	
C 13	71.2	5.9	434	4	US-09-949-016-4686	Sequence 4686, Ap	
C 14	71.2	5.9	439	4	US-09-814-915A-87	Sequence 87, Appl	
C 15	71.2	5.9	860	4	US-09-919-172-101	Sequence 101, Appl	
C 16	71.2	5.9	860	4	US-09-876-594-466	Sequence 466, App	
C 17	69	5.8	205	4	US-09-513-999C-14895	Sequence 14895, A	
C 18	65.2	5.4	1081	4	US-09-566-921-119	Sequence 119, App	
C 19	63.6	5.3	962	4	US-09-919-039-183	Sequence 183, App	
C 20	62.2	5.2	279	4	US-09-513-9990-1413	Sequence 1413, App	
C 21	54.4	4.5	2592	4	US-09-949-016-2162	Sequence 2162, A	
C 22	54.4	4.5	43690	4	US-09-949-016-11304	Sequence 11304, Ap	
C 23	54.2	4.5	421	3	US-08-643-597-308	Sequence 308, App	
C 24	54.2	4.5	421	4	US-09-480-684A-308	Sequence 308, App	
C 25	54.2	4.5	421	4	US-09-542-615A-308	Sequence 308, App	
C 26	54.2	4.5	421	4	US-09-606-421B-308	Sequence 308, App	
C 27	54.2	4.5	421	4	US-09-630-940B-308	Sequence 308, App	

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QY 301 GTGAGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 350 GTGAGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291
QY 361 TCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCA 420
Db 290 TCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCA 231
QY 421 GGAACCTCCTTTTCCATGAGTACTCTCAGTCTCTCCTTTGTTAAGTAGCCCTTTATCCCCA 480
Db 230 GGAACCTCCTTTTCCATGAGTACTCTCAGTCTCTCCTTTGTTAAGTAGCCCTTTATCCCCA 171
QY 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGCGTTCCTATTTGAGATGCAAT 540
Db 170 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGCGTTCCTATTTGAGATGCAAT 111
QY 541 TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGCGGACGCTGGGCGAGCTGGGCGAG 600
Db 110 TTGGTGTGGTCCGTTGAAGCCTTTGG-CGAGGCGCGCGGACGCTGGGCGAGCTGGGCGAG 52
QY 601 CTGAGCGCGGGCGGAGCGGAGCGGAGC 625
Db 51 CTGAGCGCGGGCGGAGCGGAGCGGAGC 27

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RESULT 2

US-09-461-912A-24/c

; Sequence 24, Application US/09461912A

; Patent No. 6709855

; GENERAL INFORMATION:

; APPLICANT: Stanton, Lawrence A.

; APPLICANT: White, R. Tyler

; APPLICANT: Damm, Deborah L.

; APPLICANT: Lewicki, John A.

; TITLE OF INVENTION: Methods for detection and use of

; TITLE OF INVENTION: differentially expressed genes in disease states

; FILE REFERENCE: SCIOS.011A

; CURRENT APPLICATION NUMBER: US/09/461,912A

; CURRENT FILING DATE: 1999-12-15

; PRIOR APPLICATION NUMBER: US 60/113,008

; PRIOR FILING DATE: 1998-12-18

; NUMBER OF SEQ ID NOS: 48

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 24

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-461-912A-24

Query Match 46.58; Score 557; DB 4; Length 579;

Best Local Similarity 99.7%; Pred. No. 1.1e-136;

Matches 579; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

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QY 1 GGAACAAAAAGAACTTTATTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 579 GGAACAAAAAGAACTTTATTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 520
QY 61 AAGCTTATCTGGATTAACTTTTCTCTGCTGTGCAAAATGAGAGTTAGATTTTATT 120
Db 519 AAGCTTATCTGGATTAACTTTTCTCTGCTGTGCAAAATGAGAGTTAGATTTTATT 460
QY 121 TTTACATTTCTAAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGAAGCTGTGG 180
Db 459 TTTACATTTCTAAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGAAGCTGTGG 400
QY 181 GCAGATTCCTTAAGCGACCTTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATT 240
Db 399 GCAGATTCCTTAAGCGACCTTTT-GGACAACTTTATCAGGAGGAGCGAACTGCTCATT 341
QY 241 TCTGCCTACTCTTTCCCTTCTGCTTCATGTGTAACAAAAATAGTCATTCGATGCAATG 300
Db 340 TCTGCCTACTCTTTCCCTTCTGCTTCATGTGTAACAAAAATAGTCATTCGATGCAATG 281

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QY 301 GTGAGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 280 GTGAGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 221
QY 361 TCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCA 420
Db 220 TCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCA 161
QY 421 GGAACCTCCTTTTCCATGAGTACTCTCAGTCTCTCCTTTGTTAAGTAGCCCTTTATCCCCA 480
Db 160 GGAACCTCCTTTTCCATGAGTACTCTCAGTCTCTCCTTTGTTAAGTAGCCCTTTATCCCCA 101
QY 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGCGTTCCTATTTGAGATGCAAT 540
Db 100 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGCGTTCCTATTTGAGATGCAAT 41
QY 541 TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGCGGAC 581
Db 40 TTGGTGTGGTCCGTTGAAGCCTTTGG-CGAGGCGCGCGGAC 1

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RESULT 3

US-09-513-999C-14898/c

; Sequence 14898, Application US/09513999C

; Patent No. 6783961

; GENERAL INFORMATION:

; APPLICANT: Dumas Milne Edwards, J.B.

; APPLICANT: Duclert, A.

; APPLICANT: Giordano, J.Y.

; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

; Patent No. 6783961

; FILE REFERENCE: 59.US2.REG

; CURRENT APPLICATION NUMBER: US/09/513,999C

; CURRENT FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/122,487

; PRIOR FILING DATE: 1999-02-26

; NUMBER OF SEQ ID NOS: 36681

; SOFTWARE: Patent.pm

; SEQ ID NO 14898

; LENGTH: 582

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 2

; OTHER INFORMATION: n=a, g, c or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 114

; OTHER INFORMATION: y=c or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 117

; OTHER INFORMATION: k=g or t

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 126

; OTHER INFORMATION: r=a or g

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: 140

; OTHER INFORMATION: r=a or g

US-09-513-999C-14898

Query Match 43.6%; Score 523; DB 4; Length 582;

Best Local Similarity 97.9%; Pred. No. 9.6e-128;

Matches 547; Conservative 4; Mismatches 4; Indels 4; Gaps 2;

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QY 30 GGAAGGGGATGCAAAACAATACAAAAATCAAAAGCTTATCTGGTATTTTAACTTTCTTTC 89
Db 582 GGAAGGGGATGCAAAACAATACAAAAATCAAAAGCTTATCTGGTATTTTAACTTTCTTTC 523

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; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Rattus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52)..(336)

US-09-399-913-64

Query Match

Best Local Similarity 27.5%; Score 329.8; DB 3; Length 600;

Matches 458; Conservative 0; Mismatches 107; Indels 24; Gaps 4;

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QY 7 AAAAAAGACTTTATTTATTTAGAGGCAAGGGGATGCAAAACAATACAAAAATCAAAAGCTT 66
Db 569 AAAAAAGACTTTCTTTATTTAGAGGCAACCGGATGCAAAACAATATAAAATCGAAAGCTC 510
QY 67 ATCTGGTAT-----TTAACTTTTCTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTT 122
Db 509 CTCTGTCATTGGATTAACTTTCTCTCTGCTTGTCAAAATGAGAGTTGGAGTTGATGTTATTG 450
QY 123 TACATTTGCTAAGTGCTGATCTGCTCATGAATCCTTCTATGGGGGAAGCTGTGGGGC 182
Db 449 CACATTTCTAAGGCTGCTGATCTGCTCA-----CAGGAAGCAGTGGGGC 405
QY 183 AGATTCTTAAGGACCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTTC 242
Db 404 AGATTCTCAGTTGACCCCATGGGAGGAGCGCATCAAGGTGTGGGTACCAAGGC-----T 349
QY 243 TGCCTACTTCTTCCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 348 CCAGTTGGCCTACTTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289
QY 303 GAGCCCGCGCAATTAGGAAAGAGCTCTGGAAGCCCACTTTTGCCTCATCTACACTGGTC 362
Db 288 GAGCCCGCGCACTAGTATGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACCTGGTC 229
QY 363 CAGTCTCTCATTTATTTTGTCCAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 422
Db 228 CAGTCTCTCATTTATTTTGTCCAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 169
QY 423 GAATTTGTAAATGTAACATCATGTTTCCATGGCGTGTTCATTTGATGATGCGCATTTT 542
Db 108 AAACCTGTGAATGTAAGCATCATGTTTCCATGGCATGCTCCATTTGGATGGCATTTT 49
QY 543 GGTGTGTCGTTGAAGCCTTGGCCGAGCGCGGCGGACGCTGGCGAG 591
Db 48 GAAG-AATCTGTTGAAACCTGGGCCCTGAGCGCTGCAGTCTTTTGAAG 1
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RESULT 6

US-09-350-614-64/c

; Sequence 64, Application US/09350614

; Patent No. 6689581

; GENERAL INFORMATION:

; APPLICANT: Rhodes, Kenneth

; APPLICANT: Betty, Maria

; APPLICANT: Ling, Hui-Ping

; APPLICANT: An, Wenqian

; TITLE OF INVENTION: POTASSIUM CHANNEL INTERACTORS AND USES THEREFOR

; FILE REFERENCE: MNI-070CP

; CURRENT APPLICATION NUMBER: US/09/350.614

; CURRENT FILING DATE: 1999-07-09

; EARLIER APPLICATION NUMBER: USSN 09/298,731

; EARLIER FILING DATE: 1999-04-23

; EARLIER APPLICATION NUMBER: USSN 60/110,277

; EARLIER FILING DATE: 1998-11-30

; EARLIER APPLICATION NUMBER: USSN 60/110,033

; EARLIER FILING DATE: 1998-11-25

; EARLIER APPLICATION NUMBER: USSN 60/109,333

; EARLIER FILING DATE: 1998-11-20

; NUMBER OF SEQ ID NOS: 72

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 64

; LENGTH: 600

; TYPE: DNA

; ORGANISM: Rattus sp.

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (52)..(336)

US-09-350-614-64

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QY 7 AAAAAAGACTTTATTTATTTAGAGGCAAGGGGATGCAAAACAATACAAAAATCAAAAGCTT 66
Db 569 AAAAAAGACTTTCTTTATTTAGAGGCAACCGGATGCAAAACAATATAAAATCGAAAGCTC 510
QY 67 ATCTGGTAT-----TTAACTTTTCTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTT 122
Db 509 CTCTGTCATTGGATTAACTTTCTCTCTGCTTGTCAAAATGAGAGTTGGAGTTGATGTTATTG 450
QY 123 TACATTTGCTAAGTGCTGATCTGCTCATGAATCCTTCTATGGGGGAAGCTGTGGGGC 182
Db 449 CACATTTCTAAGGCTGCTGATCTGCTCA-----CAGGAAGCAGTGGGGC 405
QY 183 AGATTCTTAAGGACCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTTC 242
Db 404 AGATTCTCAGTTGACCCCATGGGAGGAGCGCATCAAGGTGTGGGTACCAAGGC-----T 349
QY 243 TGCCTACTTCTTCCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 348 CCAGTTGGCCTACTTCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 289
QY 303 GAGCCCGCGCAATTAGGAAAGAGCTCTGGAAGCCCACTTTTGCCTCATCTACACTGGTC 362
Db 288 GAGCCCGCGCACTAGTATGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACCTGGTC 229
QY 363 CAGTCTCTCATTTATTTTGTCCAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 422
Db 228 CAGTCTCTCATTTATTTTGTCCAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 169
QY 423 GAATTTGTAAATGTAACATCATGTTTCCATGGCGTGTTCATTTGATGATGCGCATTTT 542
Db 108 AAACCTGTGAATGTAAGCATCATGTTTCCATGGCATGCTCCATTTGGATGGCATTTT 49
QY 543 GGTGTGTCGTTGAAGCCTTGGCCGAGCGCGGCGGACGCTGGCGAG 591
Db 48 GAAG-AATCTGTTGAAACCTGGGCCCTGAGCGCTGCAGTCTTTTGAAG 1
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RESULT 7

US-09-461-912A-23/c

; Sequence 23, Application US/09461912A

; Patent No. 6709855

; GENERAL INFORMATION:

; APPLICANT: Stanton, Lawrence A.

; APPLICANT: White, R. Tyler

; APPLICANT: Damm, Deborah L.

; APPLICANT: Lewicki, John A.

; TITLE OF INVENTION: Methods for detection and use of

; FILE REFERENCE: SCIOS.011A

; CURRENT APPLICATION NUMBER: US/09/461,912A

; CURRENT FILING DATE: 1999-12-15

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; PRIOR APPLICATION NUMBER: US 60/113,008
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 48
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 23
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Rattus rattus
US-09-461-912A-23

Query Match      27.4%; Score 328.4; DB 4; Length 570;
Best Local Similarity 78.4%; Pred. No. 1.7e-76;
Matches 453; Conservative 0; Mismatches 101; Indels 24; Gaps 4;

Qy 7 AAAAAAGAACTTTATTTATTGAGGCAAGGGATGCAAAACAATAAATAAATAAAGCTT 66
Db 561 AAAAAAGAACTTTCTTTATTGAGGCAAGGGATGCAAAACAATAAATAAATAAAGCTC 502
Qy 67 ATCTGGTAT-----TTAACTTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTTATTTT 122
Db 501 CTCTGTCAATTGGATTAACCTTTTCTCTGCTGTGCAATTTGGAGTTGATGTTATTTG 442
Qy 123 TACATTTGCTAAGTGTCTGATCTGCTCATGAATCTTCTATGGGGAAGCTGTGGGC 182
Db 441 CACATTTCTAAGGTCCTGATCTGCTCA-----CAGGAAGCAGTGGGC 397
Qy 183 AGATTCTTTAAGGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTT 242
Db 396 AGATTCTCTAGTTCAGCCCATGGGAGGAGCGCATCAAGGTGTGGTACCAGGC-----T 341
Qy 243 TGCCTACTTTCTTCTCTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 302
Db 340 CCAGTTGGCCCTACTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 281
Qy 303 GAGCCCGCAATAGGGAAGAGCTCTGCAAGCCCACTTTGCCATCTCTACACTGCTC 362
Db 280 GAGCCCGCCCACTAGTGAAGAGCTCTGCAAGCCCACTTTGCCATCTCTACACTGCTC 221
Qy 363 CAGGTCCTTCAATTTTGTCCACAGCAGAGGCTCTTTTGAATTTCCAAAAATCCAGG 422
Db 220 CAGGTCCTTCAATTTTGTCCACAGCAGAGGCTCTTTTGAATTTCCAAAAATCCAGG 161
Qy 423 GAATCTCTTTTCCATGAGTACTCTCAGGTCCTCTCTTGTGTTAAGTAGCTTTATCCCGC 482
Db 160 GAATCTCTTTTCCATGAGTACTCTCAGGTCCTCTCTTGTGTTAAGTAGCTTTATCCCGC 101
Qy 483 GAATTTGGAATGAATCAATCATGTTTCCATGCGGTGTTCCATTTGAGATGCAATTTT 542
Db 100 AAACCTGTGAATGTAAGCATCATGGTTTCCATGGCATGCTCCATTTGGGATGCAATTT 41
Qy 543 GGTGTGTCCTTGAAGCTTTGGCGGCGGCGGCGGA 580
Db 40 GAAG-AATCTGTTGAACCTGGGCGCTGCA 4

RESULT 8
US-09-313-294A-4020/c
; Sequence 4020, Application US/09313294A
; Patent No. 6476212
; GENERAL INFORMATION:
; APPLICANT: Ialguidi, Raghunath V.
; APPLICANT: Ito, Laura Y.
; APPLICANT: Sherman, Bradley K.
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR
; FILE REFERENCE: PL-0017 US
; CURRENT APPLICATION NUMBER: US/09/313,294A
; CURRENT FILING DATE: 1999-05-14
; NUMBER OF SEQ ID NOS: 7600
; SOFTWARE: PERL Program
; SEQ ID NO 4020
; LENGTH: 276
; TYPE: DNA
; ORGANISM: Zea mays

; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6476212 700347548H1
; NAME/KEY: unsure
; LOCATION: 70
; OTHER INFORMATION: a, t, c, g, or other
US-09-313-294A-4020

Query Match      13.7%; Score 164.8; DB 4; Length 276;
Best Local Similarity 79.9%; Pred. No. 1.4e-33;
Matches 218; Conservative 0; Mismatches 53; Indels 2; Gaps 2;

Qy 320 AAAAAAGCTCTGGAAGCCCACTTTTGCATCTCTACACTGCTGTCAGGTCCTTCATTTT 379
Db 276 ATAGAAAGCTCTGGAAGCCCACTTT-CCATCTCGGCACTGCTGTCAGGTCCTTCATTTT 218
Qy 380 TGTCACAGCAGAGGCTCTTTTG-ATTTTCCAAAATCCAGGGAACCTCTTTTCCATG 438
Db 217 TGTCACAGCAGAGGCTCTTTTGAATTTTCCAAAATCCAGGGAACCTCTTTTCCATG 158
Qy 439 AGTACTCTCAGGTCCTCTTTTGTAGTAGCCTTTATCCCGCAGCAATTTGTGAAATGTA 498
Db 157 AGCATCTCTCAGGTCCTCTTTTGTAGTAGTCTTTTCCCGTGCACAACTGTGAAATGTA 98
Qy 499 AACATCATGTTTCCATGCGGTGTTCATTTGAGATGGCAATTTTGTGTGTCGTTGAA 558
Db 97 AGCATCATGTTTCCATGCGGTGTTCATTTTGGATGGCAATTTTGAAGAATCTGTTGAA 38
Qy 559 GCCTTGGCCGAGGCGGCGGCGGCGGAGCTGGGCGAG 591
Db 37 ACCTGGGCCCTGAGGCGCTGCAGTCTTTTGAAG 5

RESULT 9
US-09-385-982-150
; Sequence 150, Application US/09385982
; Patent No. 6262334
; GENERAL INFORMATION:
; APPLICANT: ENDEGE, WILSON O., ET AL.
; TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION
; TITLE OF INVENTION: PRODUCTS: 11
; FILE REFERENCE: CCDNA-260XX
; CURRENT APPLICATION NUMBER: US/09/385,982
; CURRENT FILING DATE: 1999-08-30
; EARLIER APPLICATION NUMBER: 09/328,111
; EARLIER FILING DATE: 1999-06-08
; EARLIER APPLICATION NUMBER: 60/117,393
; EARLIER FILING DATE: 1999-01-27
; EARLIER APPLICATION NUMBER: 60/098,639
; EARLIER FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 544
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)...(509)
; OTHER INFORMATION: n = A,T,C or G
US-09-385-982-150

Query Match      13.7%; Score 164.8; DB 3; Length 509;
Best Local Similarity 70.9%; Pred. No. 1.9e-33;
Matches 195; Conservative 0; Mismatches 79; Indels 1; Gaps 1;

Qy 1 GGAACATAAAAGAACTTTATTTATTGAGGCAAGGGATGCAAAACAATAAATAAATCAA 60
Db 5 GGAANNAAAAAAACTTTTCTTTTGGGNNNGGNTGNCNANCNATNCAAAAAATCAA 64
Qy 61 AAGCTATCTGGTATTAACTTTTCTCTCTGCTGTGCAATGAGAGTTAGATTTTATTT 120
Db 65 AANCNTNTTGGGTTTAACTTTTCTCTCTGCTGTGCAATGAGAGTTAGATTTTATTT 124

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QY 458 TTGTTAAG 465
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Db 523 TGGTCAGG 516

RESULT 16
US-09-976-594-466/c
; Sequence 466, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 466
; LENGTH: 860
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1422432CB1
; NAME/KEY: unsure
; LOCATION: 205
; OTHER INFORMATION: a, t, c, g, or other
US-09-976-594-466

Query Match 5.9%; Score 71.2; DB 4; Length 860;
Best Local Similarity 61.2%; Pred. No. 1.1e-08;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 278 CAAATAGTCATTGTCGAATGTTGAGCGCGCAATTAGGAAAGAAAGCTCTGGAAGC 337
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Db 703 CAAAGTACTTGTGACAGCGACAGTGATTCAGCGCACGACAGATGAATCACTGAAGT 644

QY 338 CCACCTTGGCATCTCTACACTGGTCCAGGTCCTTCATATTTTTGCACAGCCAGAGGGT 397
    |||||
Db 643 CCACCTGGGCATCTCCATTGGCGTCCAGGTCCTTGAGCAATTTATCCAGGCGATCCTTGT 584

QY 398 CTTTTCGATTTCCAAAATCCAGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCCT 457
    |||||
Db 583 CTTTTCGACTCTGAGGAAGCGCTGGTAGCTCCTTCTCCATCAGCACACCTTGAGCTCCCCCT 524

QY 458 TTGTTAAG 465
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Db 523 TGGTCAGG 516

RESULT 17
US-09-513-999C-14895/c
; Sequence 14895, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 14895
; LENGTH: 205

QY 458 TTGTTAAG 465
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Db 523 TGGTCAGG 516
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 53
; OTHER INFORMATION: n=a, g, c or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 54
; OTHER INFORMATION: n=a, g, c or t
US-09-513-999C-14895

Query Match 5.8%; Score 69; DB 4; Length 205;
Best Local Similarity 88.2%; Pred. No. 2e-08;
Matches 75; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 338 CCACCTTGGCATCTCTACACTGGTCCAGGTCCTTCATATTTTTGTCCACAGCCAGAGGGT 397
    |||||
Db 205 CCACCTTGGCATCTCTACACTGGTCCAGGTCCTTCATATTATTGTCCACAGCCAGAGGGT 146

QY 398 CTTTTCGATTTCCAAAATCCAGG 422
    |||||
Db 145 CTTTTCGACACGCTATGCTCCAAG 121

RESULT 18
US-09-566-921-119/c
; Sequence 119, Application US/09566921
; Patent No. 6682888
; GENERAL INFORMATION:
; APPLICANT: Loring, Jeanne F.
; APPLICANT: Tingley, Debra W.
; APPLICANT: Edwards, Carla M.
; TITLE OF INVENTION: GENES EXPRESSED IN ALZHEIMER'S DISEASE
; FILE REFERENCE: PA-0024 US
; CURRENT APPLICATION NUMBER: US/09/566,921
; CURRENT FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 138
; SOFTWARE: PERL Program
; SEQ ID NO 119
; LENGTH: 1081
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6682888 021192.8
US-09-566-921-119

Query Match 5.4%; Score 65.2; DB 4; Length 1081;
Best Local Similarity 55.2%; Pred. No. 4.5e-07;
Matches 127; Conservative 0; Mismatches 103; Indels 0; Gaps 0;

QY 250 TTCTTTCCCTTCGTTCATGTGTACTACAAAATAGTCAATTTGCATGCAATGGTGAGGCC 309
    |||||
Db 603 TTGGCTGCTTTCTTAATCTCACTCATGTTCAAAGAACTCGTGGCAGGAGTAGTAACCATG 544

QY 310 GCAATTTAGGAAAGAAAGCTCTGGAAGCCACCTTTCGCATCTCTACACTGGTCCAGGTCC 369
    |||||
Db 543 GCAACAAAGGCCATGAATTCCTGGAAGTCAATTCGCCGCTCTCCATCATTTGTCAGTGTT 484

QY 370 TTCAATTATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCAGGGAATCC 429
    |||||
Db 483 TCCATGACTTTGTCCAAACCTCTCTCTTTGATTTTCTCTAAGAAATGGGAAAGCTCA 424

QY 430 TTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCC 479
    |||||
Db 423 TTGTTGATGAGCTCCTTTCAGTTCCGATTTCTTCAGCTTGTGCTTGTCTCC 374

RESULT 19
US-09-919-039-183/c
; Sequence 183, Application US/09919039
; Patent No. 6727066
```

; GENERAL INFORMATION:
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
; FILE REFERENCE: PA-0035 US
; CURRENT APPLICATION NUMBER: US/09/919,039
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/222,113
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 401
; SOFTWARE: PERL Program
; SEQ ID NO 183
; LENGTH: 962
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6727066 2706645CB1
US-09-919-039-183

Query Match 5.3%; Score 63.6; DB 4; Length 962;
Best Local Similarity 54.8%; Pred. No. 1.1e-06;
Matches 126; Conservative 0; Mismatches 104; Indels 0; Gaps 0;
QY 250 TTCTTTCCCTCTCTCATGCTGACTACAAATAGTCATGCAATGGTGAGGCC 309
DB 557 TTGGCTGCTTCTAACTCACTCATGTTCAAGAACTCGTGGCAGGAGTAGTAACCATG 498
QY 310 GCAATTAGGAAAAAGAGCTCTGGAAGCCACTTTGGCATCTCTACACTGCTGCAGGTCC 369
DB 497 GCAACAAGGCCATGAATCTCGAAGTCACATTCGGCGTCTCATCTATTGTCAGTGTT 438
QY 370 TTCAATATTTGTCCACAGCAGAGGCTCTTTTGTATTTTCCAAAAATCCAGGAACTCC 429
DB 437 TCCATGACTTTGTCCACAACCTCTGCTCTTTGATTTTCTTAAGAAATGGAAAGCTCA 378
QY 430 TTTTCCATGACTACTCTCAGGTCTCTCTTTGTTAAGTAGCCTTTATCCC 479
DB 377 TTGTTGATGAGCTCTTGGAGTTCGGATTCTTCACTGCTTGCTGTCTCC 328

RESULT 20
US-09-513-999C-1413/C
; Sequence 1413, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO 1413
; LENGTH: 279
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 56..277
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 223
; OTHER INFORMATION: w=a or t
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: 56
; OTHER INFORMATION: Xaa=Lys or Asn
US-09-513-999C-1413

Query Match 5.2%; Score 62.2; DB 4; Length 279;
Best Local Similarity 66.2%; Pred. No. 1.5e-06;
Matches 88; Conservative 1; Mismatches 44; Indels 0; Gaps 0;
QY 333 GAAGCCCACTTTGCCCATCTCTACATGCTCCAGGTCTCTTATTTTGTCCACAGCCAG 392
DB 268 GAAGTCCACCTGGGCATCTCCATTGGCGTCCAGGTCTTGAGCAATTTATCCACGGCATC 209
QY 393 AGGTCTTTTGTATTTTCCAAAAATCCAGGAACTCTCTTTTCCATAGTAGTACTCTCAGGTC 452
DB 208 CTGTCTTTTCCACTCTGAGGAAGCTGTAGTCTCTTCTCCATCAGCACCTTGAGCTC 149
QY 453 CTCCTTTGTTAAG 465
DB 148 CCCCTTGGTCAGG 136
RESULT 21
US-09-949-016-2162/c
; Sequence 2162, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2162
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2162

Query Match 4.5%; Score 54.4; DB 4; Length 2592;
Best Local Similarity 51.0%; Pred. No. 0.00047;
Matches 153; Conservative 0; Mismatches 146; Indels 1; Gaps 1;
QY 538 ATTTTGTGTGTCCTTGAAGCTTTGGCCGAGCGCGCGGAGCTGCGCCTTCTTTAGTACGTGC 597
DB 506 ATGTAGAGGGTGTGCGCCCGAGGCCATGGCTGAGGGTCTCCGCCCCACGCGCGCGGCC 447
QY 598 GAGCTGGACGCGGGCGGAGAGCGGCGGGCTGTGCGCCTTCTTTAGTACGTGC 657
DB 446 TCGCTCTCTGCTGCGGGCGGCGGCGGAGGAGCGGCGCGCGCTGTGGGGAAGGAAGCA 387
QY 658 GCGCGGTGGGTAGAGGAGCGCGCGGAGAGCGGAGAGACCTTGGCGGGCGCTCGGCAGG 717
DB 386 GAGGAGGAAGCGCGGAGCGGCGGGGAGAGGGGCGGGCGGCGGAGGGGCGG 327
QY 718 GCGCTCCCCAGCCCTGTCTCTCCCTCTTCTGCCCCCGACTCCCGCGACCCCGGGC 777
DB 326 GCGCCGCGGCGGCGGGGCTTCCCGCCTCTCGCTCGGTCGCGCGCGCGCGCGC 267
QY 778 GCGC-GGCCACGCCCTGCGCTCCCGGACCCCGCTCGCAGAGGCGCTCGCCCCCGCC 836
DB 266 TCGCTCGCGCGTGTCTGCTCGGCTCCCGCTCGCTCGCTCGCCGCAACCGCCGC 207
RESULT 22
US-09-949-016-13904/c
; Sequence 13904, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:

```
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CU001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: Fast-SEQ for Windows Version 4.0
; SEQ ID NO 13904
; LENGTH: 43690
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-13904

Query Match      4.5%; Score 54.4; DB 4; Length 43690;
Best Local Similarity 51.0%; Pred. No. 0.0018;
Matches 153; Conservative 0; Mismatches 146; Indels 1; Gaps 1;

QY 538 ATTTTGTGTGGTCCGTTGAAGCCTTGGCGAGCGCGCGGACGCTGGGCGAGCTGGGC 597
DB 2506 ATGTAGAGGTGTTCGCCGAGGCGATGGCTGAGGGCTCCCGCGCACGCGCGGCGCC 2447

QY 598 GAGCTGGACCGGGCGGCGAGCGAGCGCGCGGCTGTGCGCCTTCTCTTAGTACGTGC 657
DB 2446 TCGCTCCTCGCTGCGCGCGGCGGCGGAGGAGGCGCGCGCGGTGGGGAAGGCA 2387

QY 658 GCGGGTGGTAGAGGAGCGCGCGGAGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 717
DB 2386 GAGGGAGGAAGCGCGAGCGCGCGGCGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2327

QY 718 GCGTCCCGCCAGCGCTGTCTCTCCCGCTTCTCTGCGCCCGGACTCCCGCGACCCCGGC 777
DB 2326 GCGCGCGGCGGCGGCGGCGCTTCCCGCGCTTCTCTGCGCTCGGTGCGCGCGCGCGC 2267

QY 778 GCGC-GCGCCAGCGCTTCCCTCGCTTCCCGAGACCGCGCTCGCAGAGCGCTTGC CGCGCC 836
DB 2266 TCGCTCGCGCGCTGCTGCTCTCGGCTCCCGCGCTCGGCTCGGCTCGCGCAACCGCGCGC 2207

RESULT 23
US-09-643-597-308/c
; Sequence 308, Application US/09643597
; Patent No. 6426072
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C11
; CURRENT APPLICATION NUMBER: US/09/643,597
; CURRENT FILING DATE: 2000-08-21
; NUMBER OF SEQ ID NOS: 369
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-643-597-308
```

```
Query Match      4.5%; Score 54.2; DB 3; Length 421;
Best Local Similarity 51.1%; Pred. No. 0.0023;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTTCTGCGCTACTTCTTCCCTTCTCTCATGTGTACTACAAAATAGTCATTGCGATGCA 297
DB 352 AGTTTTTCATTTCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAAATTCGTTTACACATC 293

QY 298 ATGGTGAGGCCCGCAATTTAGGGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
DB 292 ATGGCGATGCAGGACAGGAAGACACAGTACTCTTTGGAAGTCCACCTCGTTTCCCTGTTG 233

QY 358 TGGTCCAGGTCCTTCAATTAATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAT 417
DB 232 CTGTCCAAGTTGCTCATCAGCTTCTGGAAGAGAGCTTCATCTGCTCTTTTCCCAAGAAG 173

QY 418 CCAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTAAAGTAGCCCTTTATCC 477
DB 172 CTGGGCGAGCTCCCGGGTCAAGCAGCTCTCTTAGTTCTGACTTGTGAGCTTGAACCTTGTC 113

QY 478 -----CCAGCGAATTTTGAAATGTAAACATCATGGTTTCCATGGGTGCGGTTCATT 528
DB 112 CCCTCTTTGCCCGAGTACTTGTGGAAGTGGACACCATCACATCCAGGGGCTTCTCCAGA 53

QY 529 TGAGATGGCAT 539
DB 52 GGGCACGCCAT 42

RESULT 24
US-09-480-884A-308/c
; Sequence 308, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-480-884A-308

Query Match      4.5%; Score 54.2; DB 4; Length 421;
Best Local Similarity 51.1%; Pred. No. 0.0023;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTTCTGCGCTACTTCTTCCCTTCTCTCATGTGTACTACAAAATAGTCATTGCGATGCA 297
DB 352 AGTTTTTCATTTCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAAATTCGTTTACACATC 293

QY 298 ATGGTGAGGCCCGCAATTTAGGGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
DB 292 ATGGCGATGCAGGACAGGAAGACACAGTACTCTTTGGAAGTCCACCTCGTTTCCCTGTTG 233

QY 358 TGGTCCAGGTCCTTCAATTAATTTTGTCCACAGCCAGAGGGTCTTTTGATTTTCCAAAAT 417
DB 232 CTGTCCAAGTTGCTCATCAGCTTCTGGAAGAGAGCTTCATCTGCTCTTTTCCCAAGAAG 173

QY 418 CCAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTAAAGTAGCCCTTTATCC 477
DB 172 CTGGGCGAGCTCCCGGGTCAAGCAGCTCTCTTAGTTCTGACTTGTGAGCTTGAACCTTGTC 113
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QY 478 -----CCAGCAATTTGAAATGTAACATCATGTTTCCATGGCGTGTTCATT 528
Db 112 CCCTCTTTGGCCGAGTACTTGTGAAGGTGGACACCATCATCCAGGGCCTTCTCCAGA 53
QY 529 TGAGATGGCAT 539
Db 52 GGGCAGCCCAT 42

RESULT 25
US-09-542-615A-308/c
; Sequence 308, Application US/09542615A
; Patent No. 6518256
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy R.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C8
; CURRENT APPLICATION NUMBER: US/09/542.615A
; CURRENT FILING DATE: 2000-04-14
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-542-615A-308

Query Match 4.5%; Score 54.2; DB 4; Length 421;
Best Local Similarity 51.1%; Pred. No. 0.00023;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTCTGCCTACTTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCATTCATGCA 297
Db 352 AGTTTTCATTTCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACATC 293
QY 298 ATGCTGAGGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
Db 292 ATGGCATGCGAGGACAGAAAGACACAGTACTCTTGGAAAGTCCACCTCGTTGCTCTGTG 233
QY 358 TGGTCCAGGTCCTTCATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTCCAAAAT 417
Db 232 CTGTCCAAGTGTCTCATCAGCTTCTGGAAGCAGCTTCATCTGCTCTTTTCCCCAAGAAG 173
QY 418 CCAGGGAACCTCTTTCCATGAGTACTCTCAGGTCTCTTTGTTAAGTAGCCCTTTATCC 477
Db 172 CTGGCAGCTCCCGGTCAGCAGCTCCTTTAGTTCTGACTTGTGAGCTTGAACCTTGCA 113
QY 478 -----CCAGCAATTTGAAATGTAACATCATGTTTCCATGGCGTGTTCATT 528
Db 112 CCCTCTTTGGCCGAGTACTTGTGAAGGTGGACACCATCATCCAGGGCCTTCTCCAGA 53
QY 529 TGAGATGGCAT 539
Db 52 GGGCAGCCCAT 42

RESULT 26
US-09-606-421B-308/c
; Sequence 308, Application US/09606421B
; Patent No. 6531315
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.

; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C9
; CURRENT APPLICATION NUMBER: US/09/606.421B
; CURRENT FILING DATE: 2000-06-28
; NUMBER OF SEQ ID NOS: 358
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-606-421B-308

Query Match 4.5%; Score 54.2; DB 4; Length 421;
Best Local Similarity 51.1%; Pred. No. 0.00023;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTCTGCCTACTTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCATTCATGCA 297
Db 352 AGTTTTCATTTCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTCGTTACATC 293
QY 298 ATGCTGAGGCCCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
Db 292 ATGGCATGCGAGGACAGAAAGACACAGTACTCTTGGAAAGTCCACCTCGTTGCTCTGTG 233
QY 358 TGGTCCAGGTCCTTCATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTCCAAAAT 417
Db 232 CTGTCCAAGTGTCTCATCAGCTTCTGGAAGCAGCTTCATCTGCTCTTTTCCCCAAGAAG 173
QY 418 CCAGGGAACCTCTTTCCATGAGTACTCTCAGGTCTCTTTGTTAAGTAGCCCTTTATCC 477
Db 172 CTGGCAGCTCCCGGTCAGCAGCTCCTTTAGTTCTGACTTGTGAGCTTGAACCTTGCA 113
QY 478 -----CCAGCAATTTGAAATGTAACATCATGTTTCCATGGCGTGTTCATT 528
Db 112 CCCTCTTTGGCCGAGTACTTGTGAAGGTGGACACCATCATCCAGGGCCTTCTCCAGA 53
QY 529 TGAGATGGCAT 539
Db 52 GGGCAGCCCAT 42

RESULT 27
US-09-630-940B-308/c
; Sequence 308, Application US/09630940B
; Patent No. 6737514
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C10
; CURRENT APPLICATION NUMBER: US/09/630.940B
; CURRENT FILING DATE: 2000-08-02
; NUMBER OF SEQ ID NOS: 367
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 308
; LENGTH: 421
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-630-940B-308


```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,946
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,560
; FILING DATE: 31-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: Double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-468-946-3
```

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Query Match 4.5%; Score 54.2; DB 2; Length 579;
Best Local Similarity 51.1%; Pred. No. 0.00026;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTCTGCTACTCTTTCCCTCTGCTTCACTGTGACTACAAATAGTCATTGCGATGCA 297
Db 446 AGTTTTCATTCTTCTCGGGCTGCTTATCTGGAAGCCTTCAAGAATTCGTTACACATC 387
QY 298 ATGTCAGGCGCCGAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
Db 386 ATGGCGATGACGACAGGAGACACAGTACTCTTGGAACTCCACCTGTTGCCCTGTG 327
QY 358 TGGTCAGGTCCTTCAATATTTTGTGCACAGCAGAGGGTCTTTTGAATTTCCAAAAT 417
Db 326 CTGTCCAAGTGTCTCATCAGCTTCTGGAAGCAGCTTCTGCTCTCTTTTCCCAAGAAG 267
QY 418 CCAGGGAACCTCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTAAGTAGCCCTTTATCC 477
Db 266 CTGGCAGCTCCCGGGTCAGCAGCTCTTTAGTTCTGACTTGTGAGCTTGAACCTGTCA 207
QY 478 -----CCAGCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGGTGTTCCATT 528
Db 206 CCCTCTTTGCCGAGTACTTGTGGAAGGTGACACCATCATCCAGGGCTTCTCCAGA 147
QY 529 TGAGATGGCAT 539
Db 146 GGGCAGCCCAT 136
```

```
RESULT 33
US-08-468-942-3/c
; Sequence 3, Application US/08468942
; Patent No. 5965360
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
```

```
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,942
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/190,560
; FILING DATE: 31-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 579 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; US-08-468-942-3

Query Match 4.5%; Score 54.2; DB 2; Length 579;
Best Local Similarity 51.1%; Pred. No. 0.00026;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

QY 238 ATTCTGCTACTCTTTCCCTCTGCTTCACTGTGACTACAAATAGTCATTGCGATGCA 297
Db 446 AGTTTTCATTCTTCTCGGGCTGCTTATCTGGAAGCCTTCAAGAATTCGTTACACATC 387
QY 298 ATGTCAGGCGCCGAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
Db 386 ATGGCGATGACGACAGGAGACACAGTACTCTTGGAACTCCACCTGTTGCCCTGTG 327
QY 358 TGGTCAGGTCCTTCAATATTTTGTGCACAGCAGAGGGTCTTTTGAATTTCCAAAAT 417
Db 326 CTGTCCAAGTGTCTCATCAGCTTCTGGAAGCAGCTTCTGCTCTCTTTTCCCAAGAAG 267
QY 418 CCAGGGAACCTCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTAAGTAGCCCTTTATCC 477
Db 266 CTGGCAGCTCCCGGGTCAGCAGCTCTTTAGTTCTGACTTGTGAGCTTGAACCTGTCA 207
QY 478 -----CCAGCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGGTGTTCCATT 528
Db 206 CCCTCTTTGCCGAGTACTTGTGGAAGGTGACACCATCATCCAGGGCTTCTCCAGA 147
QY 529 TGAGATGGCAT 539
Db 146 GGGCAGCCCAT 136
```

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RESULT 34
US-09-298-625-3/c
; Sequence 3, Application US/09298625
; Patent No. 6638504
; GENERAL INFORMATION:
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY THE MTS-1 GENE
; FILE REFERENCE: 78792YAI11-Z
; CURRENT APPLICATION NUMBER: US/09/298,625
; CURRENT FILING DATE: 1999-04-23
; PRIOR APPLICATION NUMBER: 08/468,942
; PRIOR FILING DATE: 1995-06-06
; PRIOR APPLICATION NUMBER: 08/190,560
; PRIOR FILING DATE: 1994-01-31
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; PRIOR APPLICATION NUMBER: 07/981,455
; PRIOR FILING DATE: 1992-11-25
; PRIOR APPLICATION NUMBER: 07/550,600
; PRIOR FILING DATE: 1990-07-09
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 3
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-298-625-3

Query Match      4.5%; Score 54.2; DB 4; Length 579;
Best Local Similarity 51.1%; Pred. No. 0.00026;
Matches 159; Conservative 0; Mismatches 143; Indels 9; Gaps 1;

Qy 238 ATTTCGTGCTACTTCTTCCCTCTCGCTTCATGTGTACTACAAAATAGTCATTCATGCA 297
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 298 ATGTGAGGCCGCAATTAGGAAAGAAAGCTCTGGAAGCCACTTTGCCATCTCTACAC 357
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 358 TGGTCCAGTCTCTCATTAATTTGTCACAGCCAGAGGCTTTTGAATTTCCAAAAT 417
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 326 CTGTCCAAAGTGTCTCATGCTTCTGGAAGCAGCTTCATCTGTCTTTTCCCAAG 267
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 418 CCAGGGAACCTCTTTTCCATGACTCTCAGGTCTCTTTGTTAAAGTACCTTTATCC 477
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 266 CTGGGAGCTCCCGGTGACGAGCTCTTTAGTTCTGACTTGTGAGCTTGAATTTGCA 207
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 478 -----CCAGCAATTTGTAATGTAACATCATGTTTCCATGGCGTGTTCATT 528
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 206 CCCTCTTTGCGGAGTACTTGTGAAGTGAGACACCATCACATCCAGGCGCTTCTCCAGA 147
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 529 TGAGATGGCAT 539
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 146 GGGCAGGCCAT 136
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387

RESULT 35
US-09-949-016-14837
; Sequence 14837, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14837
; LENGTH: 86380
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(86380)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14837

Query Match      4.5%; Score 54; DB 4; Length 86380;
Best Local Similarity 52.2%; Pred. No. 0.0031;
Matches 120; Conservative 0; Mismatches 110; Indels 0; Gaps 0;
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Qy 601 CTGACACCGGGGCGGAGAGCGGAGCGCGGGGCTGTGCGCTTCTTAGTACGTGCGGC 660
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 1651 CGGACACCGGGGCGGAGAGCGGAGCGCGGGGCTGTGCGCTTCTTAGTACGTGCGGC 1710
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 661 GGGTGGGTAGAGGAGCGCGGCGGAGCGGAGCGGAGCGGCTGCGCGGCGCTCGGCAGGCG 720
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 1711 GGAGAGATCGAAGGGCTAGTGGGGCGCGCAGCGCGGCGCGGCTGCGCTCCCC 1770
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 721 CTCCCCCAGCCCTGTCTCTCTCCCCCTCTTCTGCCCCCGGACTTCCCCGAGCCCCGGGCGC 780
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 1771 CCGCGTCTCTCTGGCGCCCTTCCCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1830
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 781 CGGCCCCAGCCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 830
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 1831 CCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1880
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387

RESULT 36
US-08-190-560-1/c
; Sequence 1, Application US/08190560
; Patent No. 5798257
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukanidin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 7879ZY
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-190-560-1

Query Match      4.4%; Score 53.2; DB 1; Length 303;
Best Local Similarity 51.3%; Pred. No. 0.00036;
Matches 155; Conservative 0; Mismatches 138; Indels 9; Gaps 1;
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Qy 247 TACTTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 306
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 302 TTCTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 243
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 307 CCGCAATTAGGAAAGAGAGCTCTGGAAGCCACTTGGCCATCTCTACACTGCTCCAGG 366
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
Qy 242 CAGGACAGGAAGACACAGTACTCTTGGAAAGTCCACCTCGTTGCTGCTGCTCAAG 183
Db |||||TCTTCTCTCTGGCTGCTTATCTGGGAAGCCTTCAAGAATTCGTTACATC 387
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367	TCCTTCATTTATTTTTCACAGGAGGGTCTTTTTCATTTTCCAAAAATCCAGGGAAC	426
182	TTGCTCATCAGCTTCTGGAAAGCAGCTTCATCTGTCTCTTTTCCCAAGAAGCTGGGCAGC	123
427	TCCTTTTCCATGAGTACTCTCAGGTCCCTCTGTGTTAAGTAGCCCTTTATCCCCAGC----	482
122	TCCCGGGTCAGCAGCTCCTTTTAGCTCTGACTGTGTAGCTTGAACCTTGTCAACCTCTTTTG	63
483	-----GAAATTGTGAAATGTAACATCATGGTTTCCATGGCGTGTCCATTTTGAGATGGC	537
62	CCCGAGTACTTGTGGNAGTGACACACATCACATCCAGGGCCCTTCTCCAGGGGCACGCC	3
538	AT 539	
2	AT 1	
Db	Db	

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RESULT 37
US-08-469-277-1/c
; Sequence 1, Application US/08469277
; Patent No. 5801142
; GENERAL INFORMATION:
; APPLICANT: Zain, Sayeeda
; APPLICANT: Lukandin, Eugene
; TITLE OF INVENTION: DIAGNOSIS OF METASTATIC CANCER BY
; TITLE OF INVENTION: THE MTS-1 GENE
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: United States
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,277
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/190,560
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Digiglio, Frank S.
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 78792Y
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; TELEX: 230 901 SANS UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 303 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-469-277-1

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	Query Match	4.4%	Score 53.2	DB 1	Length 303
	Best Local Similarity	51.3%	Pred. No. 0.00036		
	Matches 155	Conservative 0	Mismatches 138	Indels 9	Gaps 1
Qy	247	TACTTCTTTCCCTTCTGCTTCATCTGTGTACATACAAATAGTCATTGTCATGCAATCGTCAGG	306		
Db	302	TTCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAAATTCGTTACACATCATGCCGATG	243		
Qy	307	CCGCGCAATTAGGGAAAAAGAACTCTGGAAGCCCACTTTGGCCATCTCTACACTGCTCCAGG	366		

Db	242	CAGGACAGGAAGACACAGTACTTTGGAAGTCCACCTCGTTGTCCTGTTGCTGTCCAAG	183
Qy	367	TCCTTTCATTTATTTGTCCACAGCCAGAGGGCTTTTGTATTTTCCAAAATCCAGGGAAC	426
Db	182	TTGCTCATCAGCTTCTGGAAGCAGCTTCATCTGTCTTTTCCCAAGAACTGGGCAGC	123
Qy	427	TCCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGGCTTTATTCGCCAGC----	482
Db	122	TCCCGGGTCACAGCTCCTTTAGCTCTCACTTGTGTGAGCTTGAACCTGTGCACCCCTCTT	63
Qy	483	-----GAATTTGTGAATGAAACATCATGTTTCCATGGCGTGTTCCATTTTGAGATGGC	537
Db	62	CCCGAGTACTTGTGGAAGGTGGACACCATCATCCAGGGCCCTCTCCAGAGGGCAGGCC	3
Qy	538	AT 539	
Db	2	AT 1	

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	Query Match	4.4%	Score 53.2;	DB 2;	Length 303;
	Best Local Similarity	51.3%;	Pred. No. 0.00036;		
	Matches 155;	Conservative 0;	Mismatches 138;	Indels 9;	Gaps 1
Qy	247	TACTTCTTCCCTTCTCTCTCATGTGTACTACAAAAATAGTTCATTGCGATGCAATGGTGGG	306		
Db	302	TTCTTCTGGGCTCTTATCTGGGAAGCCTTCAAAGAAATTCGTTACACATCATGGCGATG	243		

RESULT 42
US-08-322-742-1/C

```

; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darriek
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C14
; CURRENT APPLICATION NUMBER: US/09/702.705
; CURRENT FILING DATE: 2000-10-30
; NUMBER OF SEQ ID NOS: 1833
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1585
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-702-705-1585

Query Match      4.4%; Score 52.6; DB 4; Length 392;
Best Local Similarity 50.8%; Pred. No. 0.00058;
Matches 158; Conservative 0; Mismatches 144; Indels 9; Gaps 1;

Qy      238  ATTTCTGCCTACTTCTTCCCTTCTGCTTCTCATGTGTACTACAAATAGTCATTCGATGCA 297
Db      364  AGTTTTCAATTCCTTCTGGGCTGCTTATCTGGGAAGCCTTCAAAGAATTGTTACACATC 305

Qy      298  ATGTGTAGGGCCGCAATTAGGGAAAAAGAAAGCTCTGGGAAGCCACTTTGCCATCTCTACAC 357
Db      304  ATGGCGATGCAGGACAGGACAGACTACTTTAGAAGTCCACTCGTTGTGCTCTGTG 245

Qy      358  TGTGTCCAGGTCTCTTCATATATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAAT 417
Db      244  CTGTGCCAAGTGTCTCATCAGCTTCTGGAAGACAGCTTCATCTGTCTCTTTTCCCAAGAAG 185

Qy      418  CCAGGGAATCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAGTAGCCCTTTATCC 477
Db      184  CTGGGCAGCTCCCGGGTCAGCAGCTCTCTTAGTTCTGACTTGTGTGAGCTTGAATCTGTCA 125

Qy      478  CCAGC-----GAATTTGTGAAATGTAAACATCATGTTTCCATGGGGTGTGTCCATT 528
Db      124  CCCTCTTTGCCCGAGTACTTGTGGAAGTGGACACCATCATACCAGGGCCTTCTCCAGA 65

Qy      529  TGAGATGGCAT 539
Db      64  GGGCAGCCAT 54

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RESULT 44
US-09-736-457-1585/c
; Sequence 1585, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1585
; LENGTH: 392
; TYPE: DNA

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; ORGANISM: Homo sapiens
US-09-736-457-1585

Query Match      4.4%; Score 52.6; DB 4; Length 392;
Best Local Similarity 50.8%; Pred. No. 0.00058;
Matches 158; Conservative 0; Mismatches 144; Indels 9; Gaps 1;

Qy 238 ATTTCTCGCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAATAGTCAATGCATGCA 297
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364 AGTTTTCAATTTCTCTCGGGCTGCTTATCTGGGAAGCCTTCAAAGAAATCGTTACACATC 305
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Qy 298 ATGCTGAGGCCCAATTAGGAAAAGAAAGCTCTGGGAAGCCACTTTGCCATCTCTACAC 357
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
304 ATGGCGATGAGGACAGGAAGACACAGTACTCTTTAGAAAGTCCACCTCGTTGTCCCTGTTG 245
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Qy 358 TGGTCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAAT 417
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
244 CTGTCCAAAGTGTCTATCAGCTTCTGGAAGCAGCTTCATCTGTCTCTTTTCCCAAGAG 185
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 418 CCAGGGAACCTCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTTAAAGTAGCCTTTATCC 477
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
184 CTGGGCAGCTCCCGGGTCAGCAGCTCTTTAGTTCTGACTTGTGTAGCTTTGAACTTGCA 125
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Qy 478 CCAGC-----GAATTTGTGAAATGTAACATCATGGTTTCCATGGCGGTGTTCCATT 528
Db      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
124 CCCTCTTTTGCCCGAGTACTTTGTGGAAGTGGACACCATCATCCAGGGCCTTCTCCAGA 65
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Qy 529 TGAGATGGCAT 539
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RESULT 45
US-09-614-124B-1585/c
; Sequence 1585, Application US/09614124B
; Patent No.: 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1585
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-614-124B-1585

Query Match      4.4%; Score 52.6; DB 4; Length 392;
Best Local Similarity 50.8%; Pred. No. 0.00058;
Matches 158; Conservative 0; Mismatches 144; Indels 9; Gaps 1;

Qy 238 ATTTCTCGCTACTTCTTTCCCTCTGCTTCATGTGTACTACAAATAGTCAATGCATGCA 297
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Qy 298 ATGCTGAGGCCCAATTAGGAAAAGAAAGCTCTGGGAAGCCACTTTGCCATCTCTACAC 357
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Qy 358 TGGTCCAGGTCCTTCATTAATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAAT 417
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244 CTGTCCAAAGTGTCTATCAGCTTCTGGAAGCAGCTTCATCTGTCTCTTTTCCCAAGAG 185
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Qy	478	CCAGC-----GAAATTTGTAATGTAAACATCATGGTTTCCATGGCGTGTTCATT	528
Db	124	CCCTCTTTGCCCGAGTACTTGTGAAGGTGGACACCATCACATCCAGGGCCTTCTCCAGA	65
Qy	529	TGAGATGGCAT	539
Db	64	GGCACGCCAT	54

Search completed: August 17, 2005, 22:33:07
Job time : 247 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 22:20:57 ; Search time 793 Seconds
(without alignments)
9823.210 Million cell updates/sec

Title: US-10-735-577-16
Perfect score: 1199
Sequence: 1 ggaactaaaaaagaacttta.....cgggcttcgcccccacggg 1199

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq.*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq.*
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- 8: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq.*
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- 10: /cgn2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq.*
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq.*
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq.*
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq.*
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq.*
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq.*
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq.*
- 19: /cgn2_6/ptodata/2/pubpna/US10G_PUBCOMB.seq.*
- 20: /cgn2_6/ptodata/2/pubpna/US10H_PUBCOMB.seq.*
- 21: /cgn2_6/ptodata/2/pubpna/US10I_PUBCOMB.seq.*
- 22: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
- 23: /cgn2_6/ptodata/2/pubpna/US11A_PUBCOMB.seq.*
- 24: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq.*
- 25: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
- 26: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1199	100.0	1199	19	US-10-735-577-16
2	1199	100.0	1199	19	US-10-735-577-16
3	703.4	58.7	1124	13	US-10-044-090-1
4	634	52.9	1893	9	US-09-925-301-586
5	634	52.9	1893	10	US-09-997-003-13
6	601	50.1	649	9	US-09-880-107-2350
7	601	50.1	649	17	US-10-172-118-847

c 8	601	50.1	649	18	US-10-342-887-847	Sequence 847, App
c 9	601	50.1	649	20	US-10-487-337-7	Sequence 7, Appli
c 10	601	50.1	649	21	US-10-956-157-979	Sequence 979, App
c 11	601	50.1	649	21	US-10-956-157-979	Sequence 6214, Ap
c 12	595.8	49.7	663	17	US-10-264-049-1114	Sequence 1114, Ap
c 13	577.4	48.2	608	13	US-10-027-632-261591	Sequence 261591,
c 14	577.4	48.2	608	17	US-10-027-632-261591	Sequence 261591,
c 15	537	44.8	571	9	US-09-920-300A-890	Sequence 890, App
c 16	537	44.8	571	13	US-10-033-528-890	Sequence 890, App
c 17	537	44.8	571	16	US-10-099-926-890	Sequence 890, App
c 18	537	44.8	571	22	US-10-961-527-890	Sequence 890, App
c 19	516	43.0	538	17	US-10-242-535A-47618	Sequence 47618, A
c 20	516	43.0	538	18	US-10-085-783A-47618	Sequence 1, Appli
c 21	485.2	40.5	2016	10	US-09-992-600A-1	Sequence 1, Appli
c 22	485.2	40.5	2016	10	US-09-924-340-1	Sequence 1, Appli
c 23	485.2	40.5	2016	10	US-09-992-095B-1	Sequence 1, Appli
c 24	485.2	40.5	2016	10	US-09-999-570-1	Sequence 1, Appli
c 25	485.2	40.5	2016	14	US-10-000-489-1	Sequence 1, Appli
c 26	485.2	40.5	2016	14	US-10-000-986-1	Sequence 1, Appli
c 27	485.2	40.5	2016	16	US-10-154-678-1	Sequence 1, Appli
c 28	485.2	40.5	2016	16	US-10-001-142-1	Sequence 1, Appli
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c 30	471.6	39.3	482	17	US-10-242-535A-46392	Sequence 46392, A
c 31	471.6	39.3	482	18	US-10-085-783A-46392	Sequence 46392, A
c 32	461.4	38.5	472	17	US-10-242-535A-57930	Sequence 57930, A
c 33	461.4	38.5	472	18	US-10-085-783A-57930	Sequence 49122, A
c 34	448	37.4	480	17	US-10-242-535A-49122	Sequence 49122, A
c 35	448	37.4	480	18	US-10-085-783A-49122	Sequence 56036, A
c 36	446.4	37.2	474	17	US-10-242-535A-56036	Sequence 56036, A
c 37	446.4	37.2	474	18	US-10-085-783A-56036	Sequence 56036, A
c 38	434.4	36.2	448	17	US-10-242-535A-56504	Sequence 56504, A
c 39	434.4	36.2	448	18	US-10-085-783A-56504	Sequence 21508, A
c 40	429.4	35.8	477	10	US-09-918-995-21508	Sequence 12556, A
c 41	422	35.2	466	10	US-09-918-995-12556	Sequence 26, Appl
c 42	411	34.3	441	10	US-09-997-003-26	Sequence 2418, Ap
c 43	396.2	33.0	632	15	US-10-106-698-2418	Sequence 45565, A
c 44	377.4	31.5	392	17	US-10-242-535A-45565	Sequence 45565, A
c 45	377.4	31.5	392	18	US-10-085-783A-45565	Sequence 45565, A

ALIGNMENTS

RESULT 1

US-10-735-577-16

; Sequence 16, Application US/10735577

; Publication No. US20040142897A1

; GENERAL INFORMATION:

; APPLICANT: Walsman, David M.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastases

; FILE REFERENCE: ME03-009

; CURRENT APPLICATION NUMBER: US/10/735,577

; CURRENT FILING DATE: 2003-12-12

; PRIOR APPLICATION NUMBER: US 60/433,140

; PRIOR FILING DATE: 2002-12-13

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: Microsoft Word

; SEQ ID NO 16

; LENGTH: 1199

; TYPE: DNA

; ORGANISM: mammalian

US-10-735-577-16

Query Match 100.0%; Score 1199; DB 19; Length 1199;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 GGAATAAAAAAGAACTTTATTATTGAGGCGGAGGATGCAACAAATACAAAAATCAA 60

Qy 61 AAGCTATCTGGTATTAACTTTCTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 120

Db 61 AAGCTTATCTGGTATTAACTTTTCTCTGCTGTCAAAATGAGAGTTAGATTTTATT 120
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Qy 961 GAACCCGGCGCTCTCGGGTGGGGCACGCTGGCGCAGAACCCAGAGGTAAACCGGCTCTGC 1020
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RESULT 2

US-10-735-577-17/c

; Sequence 17, Application US/10735577

; Publication No. US20040142897A1

; GENERAL INFORMATION:

; APPLICANT: Waisman, David M.

; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastasis

; FILE REFERENCE: ME03-009

; CURRENT APPLICATION NUMBER: US/10/735,577

; CURRENT FILING DATE: 2003-12-12

; PRIOR APPLICATION NUMBER: US 60/433,140

; PRIOR FILING DATE: 2002-12-13

; NUMBER OF SEQ ID NOS: 160

; SOFTWARE: Microsoft Word

; SEQ ID NO 17

; LENGTH: 1199

; TYPE: DNA

; ORGANISM: mammalian

US-10-735-577-17

Query Match 100.0%; Score 1199; DB 19; Length 1199;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 1199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1199 GGAACCTAAAAAGAACTTTTATTGAGGGCAAGGGATGCAAAACAATACAAAAATCAA 1140
Qy 61 AAGCTTATCTGGTATTAACTTTTCTCTCTCTGTTGTCAAATGAGAGTTAGATTTTATT 120
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Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCAT 240
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Db 719 GCGAAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAATT 660
Qy 541 TTGCTGTGGTCCGTTGAAGCCTTTGGCCAGCGCGGACGCTGGCGGAGCTGGGCGAG 600
Db 659 TTGCTGTGGTCCGTTGAAGCCTTTGGCCAGCGCGGACGCTGGCGGAGCTGGGCGAG 600
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Db 599 CTGGAACCGGGCGGAGAGCGAGCGCGGCTGTGCGGCTTCTTCTAGTACGTGCGGC 540
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Db 539 GGGTGGGTAGAGGAGCGCGGCGGAGCGGAGCGCTTCCCGCCCGCCACCGG 480

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; OTHER INFORMATION: n equals a,t,g, or c			
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; LOCATION: (1893)			
; OTHER INFORMATION: n equals a,t,g, or c			
US-09-925-301-586			
Query Match 52.9%; Score 634; DB 9; Length 1893;			
Best Local Similarity 100.0%; Pred. No. 1.le-176;			
Matches 634; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1776	AAG	CTTATCTGGTATTTAACTTTTCTTCTCTGCTGTGCAAAATGAGAGTTAGATTTTATT 1717
Qy	121	TTT	ACATTTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 180
Db	1716	TTT	ACATTTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGG 1657
Qy	181	GC	AGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCAT 240
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Qy	241	TC	TGCCTACTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTGCGATGCAATG 300
Db	1596	TC	TGCCTACTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTGCGATGCAATG 1537
Qy	301	GT	GAGGCCCGCAATTTAGGGAAGAAAGAGCTCTGGAAGGCCCACTTTGGCCATCTCTACACTGG 360
Db	1336	GT	GAGGCCCGCAATTTAGGGAAGAAAGAGCTCTGGAAGGCCCACTTTGGCCATCTCTACACTGG 1477
Qy	361	TCC	AGGTCTCTTCATTTATTTTGTCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 420
Db	1476	TCC	AGGTCTCTTCATTTATTTTGTCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 1417
Qy	421	GGG	AATCTCTTTTCGATGAGTACTCTCAGGTCTCTCTTTGTTAGTAGAGCCCTTTATCCCCA 480
Db	1416	GGG	AATCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAGTAGAGCCCTTTATCCCCA 1357
Qy	481	CG	CAATTTGTCAATGTAAACATCATGTTTCCATGGCGTGTCTCCATTTTGAGATGGCAATT 540
Db	1356	CG	CAATTTGTCAATGTAAACATCATGTTTCCATGGCGTGTCTCCATTTTGAGATGGCAATT 1297
Qy	541	TT	GTGTGTGTCCTTTGAAGCCTTTGGCCGAGCGCGCGGAGCGCTTGGCGAGCTGGGCGAG 600
Db	1296	TT	GTGTGTGTCCTTTGAAGCCTTTGGCCGAGCGCGCGGAGCGCTTGGCGAGCTGGGCGAG 1237
Qy	601	CT	GACCGGGCGGAGAGGCGAGCGCGGGCGGC 634
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RESULT 5

US-09-997-003-13/c	
; Sequence 13, Application US/09997003	
; Publication No. US20030203361A1	
; GENERAL INFORMATION:	
; APPLICANT: Rosen et al.	
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies	
; FILE REFERENCE: PA003P1	
; CURRENT APPLICATION NUMBER: US/09/997,003	
; CURRENT FILING DATE: 2001-11-30	
; PRIOR APPLICATION NUMBER: unassigned	
; PRIOR FILING DATE: 2001-11-30	
; PRIOR APPLICATION NUMBER: PCT/US00/22157	
; PRIOR FILING DATE: 2000-08-11	
; PRIOR APPLICATION NUMBER: 60/148,680	
; PRIOR FILING DATE: 1999-08-13	
; NUMBER OF SEQ ID NOS: 56	

1476	TCCAGGTCCTTCATTTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCA	1417
421	GGGAACCTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCCCA	480
1416	GGGAACCTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCCCA	1357
481	GCGAATTTCTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCAATT	540
1356	GCGAATTTCTGAAATGTAAACATCATGTTTCCATGGCGTGTTCCATTTGAGATGGCAATT	1297
541	TTGGTGTGTCCTGTTAAAGCCTTTGCCCGAGCGCGCGGACGCTGGGCGAGCTGGGCGAG	600
1296	TTGGTGTGTCCTGTTAAAGCCTTTGCCCGAGCGCGCGGACGCTGGGCGAGCTGGGCGAG	1237
601	CTGGACGCGGGGCGGAGAGGCGCGCGGGCGGC	634

601 CTGGACCGGGCGGAGAGCGAGCGCGGGC 634

Db 350 GTGAGCGCGCAATTAGGAAAGAGCTCTGGAAGCCACTTTGCCATCTCTACACTGG 291
Qy 361 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 420
Db 290 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 231
Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 480
Db 230 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 171
Qy 481 CGCAATTTGTGAATGTAAACATCATGCTTTCCATGGCTGCTTCCATTTGAGATGGCAAT 540
Db 170 CGCAATTTGTGAATGTAAACATCATGCTTTCCATGGCTGCTTCCATTTGAGATGGCAAT 111
Qy 541 TTGCTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGGAGCGCTGGGCGAGCTGGGCGAG 600
Db 110 TTGCTGTGGTCCGTTGAAGCCTTTGG-CCAGGCGCGGCGAGCGCTGGGCGAGCTGGGCGAG 52
Qy 601 CTGGACGCGGCGGCGAGAGCGAGC 625
Db 51 CTGGACGCGGCGGCGAGAGCGAGC 27

RESULT 10
US-10-956-157-979/c
; Sequence 979, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 979
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-979

Query Match 50.1%; Score 601; DB 21; Length 649;
Best Local Similarity 99.7%; Pred. No. 3.7e-167;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 GGAACCTAAAGAAAGAACTTTATTTATTTGAGGCGCAAGGGATGCAACAATACAAAAATCAA 60
Db 649 GGAACCTAAAGAAAGAACTTTATTTATTTGAGGCGCAAGGGATGCAACAATACAAAAATCAA 590
Qy 61 AAGCTTATCTGCTATTTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
Db 589 AAGCTTATCTGCTATTTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530
Qy 121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180
Db 529 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 470
Qy 121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180
Db 529 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 470
Qy 181 GCAGATTCCTTAAGGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 240
Db 469 GCAGATTCCTTAAGGACCCCTTTT-GGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 411
Qy 241 TCTGCTACTTCTTTCCCTCTGCTTCAATGTGTAATAAATAGTCAATGCAATGCAATG 300
Db 410 TCTGCTACTTCTTTCCCTCTGCTTCAATGTGTAATAAATAGTCAATGCAATGCAATG 351
Qy 301 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 350 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291
Qy 361 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 420
Db 290 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 231
Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 480

Db 290 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 231
Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 480
Db 230 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 171
Qy 481 CGCAATTTGTGAATGTAAACATCATGCTTTCCATGGCTGCTTCCATTTGAGATGGCAAT 540
Db 170 CGCAATTTGTGAATGTAAACATCATGCTTTCCATGGCTGCTTCCATTTGAGATGGCAAT 111
Qy 541 TTGCTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGGAGCGCTGGGCGAGCTGGGCGAG 600
Db 110 TTGCTGTGGTCCGTTGAAGCCTTTGG-CCAGGCGCGGCGAGCGCTGGGCGAGCTGGGCGAG 52
Qy 601 CTGGACGCGGCGGCGAGAGCGAGC 625
Db 51 CTGGACGCGGCGGCGAGAGCGAGC 27

RESULT 11
US-10-956-157-6214/c
; Sequence 6214, Application US/10956157
; Publication No. US20050118625A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William
; TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
; TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
; FILE REFERENCE: 031896-043000 (AM 101081)
; CURRENT APPLICATION NUMBER: US/10/956.157
; CURRENT FILING DATE: 2004-10-04
; NUMBER OF SEQ ID NOS: 319805
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6214
; LENGTH: 649
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-956-157-6214

Query Match 50.1%; Score 601; DB 21; Length 649;
Best Local Similarity 99.7%; Pred. No. 3.7e-167;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 GGAACCTAAAGAAAGAACTTTATTTATTTGAGGCGCAAGGGATGCAACAATACAAAAATCAA 60
Db 649 GGAACCTAAAGAAAGAACTTTATTTATTTGAGGCGCAAGGGATGCAACAATACAAAAATCAA 590
Qy 61 AAGCTTATCTGCTATTTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120
Db 589 AAGCTTATCTGCTATTTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 530
Qy 121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180
Db 529 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 470
Qy 181 GCAGATTCCTTAAGGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 240
Db 469 GCAGATTCCTTAAGGACCCCTTTT-GGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 411
Qy 241 TCTGCTACTTCTTTCCCTCTGCTTCAATGTGTAATAAATAGTCAATGCAATGCAATG 300
Db 410 TCTGCTACTTCTTTCCCTCTGCTTCAATGTGTAATAAATAGTCAATGCAATGCAATG 351
Qy 301 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 350 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 291
Qy 361 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 420
Db 290 TCCAGGTCCTTCATTTATTTGTCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAATCCA 231
Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAGTAGACCTTTATCCCCA 480

Db	230	GGGAACCTCTTTTCCATGAGTACTCTCAGGTCCTCTTTGTGTAAGTAGCCTTTATCCCCA	171
Qy	481	GGCAATTTGTGAAATGTAACATCATGTGTTTCCATGGCGTGTTCCATTTGAGATGGCATT	540
Db	170	GGCAATTTGTGAAATGTAACATCATGTGTTTCCATGGCGTGTTCCATTTGAGATGGCATT	111
Qy	541	TTGGTGTGTCCTCGTTGAAGCCTTGCCCGAGGCGGCGGACGCTGGGCGAGCTGGGCGAG	600
Db	110	TTGGTGTGTCCTCGTTGAAGCCTTGCG- CGAGGCGGCGGCGGACGCTGGGCGAGCTGGGCGAG	52
Qy	601	CTCGACGCGGGCGGAGGCGGAGC	625
Db	51	CTTGACGCGGGCGGAGGCGGAGC	27

RESULT 12

US-10-264-049-1114/c

; Sequence 1114, Application US/10264049

; Publication No. US20040005579A1

; GENERAL INFORMATION:

; APPLICANT: Birse et al.

; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies

; FILE REFERENCE: PA133P1

; CURRENT APPLICATION NUMBER: US/10/264,049

; CURRENT FILING DATE: 2002-10-04

; PRIOR APPLICATION NUMBER: PCT/US01/18569

; PRIOR FILING DATE: 2001-06-07

; PRIOR APPLICATION NUMBER: US 60/209,467

; PRIOR FILING DATE: 2000-06-07

; NUMBER OF SEQ ID NOS: 4360

; SOFTWARE: Patentin Ver. 3.1

; SEQ ID NO 1114

; LENGTH: 663

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (553)..(553)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (602)..(602)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (623)..(623)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (656)..(657)

; OTHER INFORMATION: n equals a,t,g, or c

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (661)..(661)

; OTHER INFORMATION: n equals a,t,g, or c

US-10-264-049-1114

Qy	182	CAGATTCCTTAAAGCGACCCCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTGCTCATTTT	241
Db	421	CAGATTCCTTAAAGCGACCCCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTGCTCATTTT	362
Qy	242	CTGGCTACTTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTGCATGCAATGG	301
Db	361	CTGGCTACTTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTGCATGCAATGG	302
Qy	302	TGAGGCCCGCAATTTAGGGAAAAGAGCTCTCGAAGCCCACTTTTGGCCATCTCTACACTGGT	361
Db	301	TGAGGCCCGCAATTTAGGGAAAAGAGCTCTCGAAGCCCACTTTTGGCCATCTCTACACTGGT	242
Qy	362	CCAGGTCCTTTCATTTATTTTGTCCACAGCAGCAGGGGTCTTTTGTGATTTTCCAAAAATCCAG	421
Db	241	CCAGGTCCTTTCATTTATTTTGTCCACAGCAGCAGGGGTCTTTTGTGATTTTCCAAAAATCCAG	182
Qy	422	GGAAGTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTAAAGTAGCGCTTTATCCCCAG	481
Db	181	GGAAGTCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTAAAGTAGCGCTTTATCCCCAG	122
Qy	482	CGAATTTGTGAAATGTAACAATCATGTTTCCATGGCGTGTTCACATTTTGAGATGGCATTT	541
Db	121	CGAATTTGTGAAATGTAACAATCATGTTTCCATGGCGTGTTCACATTTTGAGATGGCATTT	62
Qy	542	TGTTGTGGTCCGTTGAAAGCCTTGGCCGAGCGCGCGACGCTGGGCGAGCTTGGGCGAGC	601
Db	61	TGTTGTGGTCCGTTGAAAGCCTTGGCCGAGCGCGCGACGCTGGGCGAGCTTGGGCGAGC	2
RESULT 13			
US-10-027-632-261591/c			
; Sequence 261591, Application US/10027632			
; Publication No. US20020198371A1			
; GENERAL INFORMATION:			
; APPLICANT: wang, David G.			
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide			
; TITLE OF INVENTION: Polymorphisms in the Human Genome			
; FILE REFERENCE: 108827.129			
; CURRENT APPLICATION NUMBER: US/10/027,632			
; CURRENT FILING DATE: 2002-04-30			
; PRIOR APPLICATION NUMBER: US 60/218,006			
; PRIOR FILING DATE: 2000-07-12			
; PRIOR APPLICATION NUMBER: US 60/198,676			
; PRIOR FILING DATE: 2000-04-20			
; PRIOR APPLICATION NUMBER: US 60/193,483			
; PRIOR FILING DATE: 2000-03-29			
; PRIOR APPLICATION NUMBER: US 60/185,218			
; PRIOR FILING DATE: 2000-02-24			
; PRIOR APPLICATION NUMBER: US 60/167,363			
; PRIOR FILING DATE: 1999-11-23			
; PRIOR APPLICATION NUMBER: US 60/156,358			
; PRIOR FILING DATE: 1999-09-28			
; PRIOR APPLICATION NUMBER: US 60/146,002			
; PRIOR FILING DATE: 1999-08-09			
; NUMBER OF SEQ ID NOS: 325720			
; SOFTWARE: FastSeq for Windows Version 4.0			
; SEQ ID NO 261591			
; LENGTH: 608			
; TYPE: DNA			
; ORGANISM: Human			
US-10-027-632-261591			

		Query Match	49.7%	Score 595.8	DB 17	Length 663
		Best Local Similarity	99.5%	Prod. No. 1.3e-165		
		Matches 597	Conservative 0	Mismatches 3	Indels 0	Gaps 0
Qy	2	GAACCTAAAAGAACCTTTATTATTATGAGGCAAGGGATGCAAAACAATACAAAAATCAAA	61			
Db	601	GAACCTAAAAGAACCTTTATTATTATGAGGCAAGGGATGCAAAACAATACAAAAATCAAA	542			
Qy	62	AGCTTATCTGGTATTTTAACTTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTT	121			
Db	541	AGCTTATCTGGTATTTTAACTTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTT	482			
Qy	122	TTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGG	181			
Db	481	TTACATTTGCTAAGTGCCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGG	422			

Qy 1 GGAACATAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAATACAAAAATCAA 60
Db |||||
Qy 28 GNAACATAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAATACAAAAATCAA 87
Db |||||
Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGCTCAAAATGAGAGTTAGATTTATT 120
Db |||||
Qy 88 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGCTCAAAATGAGAGTTANATTTATT 147
Db |||||
Qy 121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 180
Db |||||
Qy 148 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 207
Db |||||
Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATT 240
Db |||||
Qy 208 GCANATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATT 267
Db |||||
Qy 241 TCTGCTACTCTTCTTCCCTTCTGCTTCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 300
Db |||||
Qy 268 TCTGCTACTCTTCTTCCCTTCTGCTTCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 327
Db |||||
Qy 301 GTGAGGCGCGCAATAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db |||||
Qy 328 GTGAGGCGCGCAATAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 387
Db |||||
Qy 361 TCCAGGCTCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 420
Db |||||
Qy 388 TCCAGGCTCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 447
Db |||||
Qy 421 GGGAACTCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTACCTTTATCCCA 480
Db |||||
Qy 448 GGGAACTCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTACCTTTATCCCA 507
Db |||||
Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCATT 540
Db |||||
Qy 508 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCATT 567
Db |||||
Qy 541 TTGG 544
Db |||||
Qy 568 TTGG 571

RESULT 18

US-10-961-527-890
; Sequence 890, Application US/10961527
; Publication No. US20050147615A1
; GENERAL INFORMATION:
; APPLICANT: King, Gordon E.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Xu, Jiangchun
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF COLON CANCER
; FILE REFERENCE: 210121.547C4
; CURRENT APPLICATION NUMBER: US/10/961,527
; CURRENT FILING DATE: 2004-10-07
; PRIOR APPLICATION NUMBER: US 09/920,300
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: US 60/302,051
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/279,763
; PRIOR FILING DATE: 2001-03-28
; PRIOR APPLICATION NUMBER: US 60/223,283
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 1789
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 890
; LENGTH: 571
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 29, 40, 139, 211, 351, 379, 559

; OTHER INFORMATION: n = A,T,C or G
US-10-961-527-890

Query Match 44.8%; Score 537; DB 22; Length 571;
Best Local Similarity 98.7%; Pred. No. 3.3e-148;
Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
Qy 1 GGAACATAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAATACAAAAATCAA 60
Db 28 GNAACATAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAATACAAAAATCAA 87
Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGCTCAAAATGAGAGTTAGATTTATT 120
Db 88 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGCTCAAAATGAGAGTTANATTTATT 147
Qy 121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 180
Db 148 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 207
Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATT 240
Db 208 GCANATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATT 267
Qy 241 TCTGCTACTCTTCTTCCCTTCTGCTTCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 300
Db 268 TCTGCTACTCTTCTTCCCTTCTGCTTCTGCTCATGAAATCCCTTCTATGGGGAAGCTGTGGG 327
Qy 301 GTGAGGCGCGCAATAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 328 GTGAGGCGCGCAATAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 387
Qy 361 TCCAGGCTCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 420
Db 388 TCCAGGCTCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA 447
Qy 421 GGGAACTCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTACCTTTATCCCA 480
Db 448 GGGAACTCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTACCTTTATCCCA 507
Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCATT 540
Db 508 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCATT 567
Qy 541 TTGG 544
Db |||||
Qy 568 TTGG 571

RESULT 19

US-10-242-535A-47618/c
; Sequence 47618, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 47618
; LENGTH: 538
; TYPE: DNA
; ORGANISM: Human

; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1435..1836
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1965..1970
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2001..2016
US-09-992-095B-1

Query Match 40.5%; Score 485.2; DB 10; Length 2016;
Best Local Similarity 94.7%; Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy	73	TATTTAACTTTCTCTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT	132
Db	2012	TTTTTTTTTTCTCTCTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT	1953
Qy	133	AAGTGCTCTGATCTGCTCATGAATCTTCTATGGGGAGAGCTGTGGGCGAGATTCCTTA	192
Db	1952	AAGTGCTCTGATCTGCTCATGAATCTTCTATGGGGAGAGCTGTGGGCGAGATTCCTTA	1893
Qy	193	AGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAITTCGCTACTTC	252
Db	1892	AGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAITTCGCTACTTC	1833
Qy	253	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGGTGGAGCCGCA	312
Db	1832	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGGTGGAGCCGCA	1773
Qy	313	ATTAGGAAAAGAGCTCTGGAAGCCACCTTGGCCATCTCTACACTGGTCCAGGTCCTTC	372
Db	1772	ATTAGGAAAAGAGCTCTGGAAGCCACCTTGGCCATCTCTACACTGGTCCAGGTCCTTC	1713
Qy	373	ATTATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAATCCTTT	432
Db	1712	ATTATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAATCCTTT	1653
Qy	433	TCCATGAGTACTCTCAGGTCCTCTTTGTTAAAGTAGCCTTTATCCCGAGCAATTTGTGA	492
Db	1652	TCCATGAGTACTCTCAGGTCCTCTTTGTTAAAGTAGCCTTTATCCCGAGCAATTTGTGA	1593
Qy	493	AATGTAAACATCATGGTTTCCATGGCGTGTTCATTTTGGATGGCATTTTGTGTGTC	552
Db	1592	AATGTAAACATCATGGTTTCCATGGCGTGTTCATTTTGGATGGCATTTTGTGTGTC	1533
Qy	553	GTTGAAGCCTTTGGCCGAGGCGCGGACGCTGGCGAGCTGGCGGAGCT 602	
Db	1532	GTTGAAGCCTTTGGCCGAGGCTCAGTGCAGGCTGTGGCGAGGCAAGAAAGGT 1483	

RESULT 24

US-09-999-570-1/c

; Sequence 1, Application US/09999570

; Publication No. US20030170628A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: G-091US08DIV
; CURRENT APPLICATION NUMBER: US/09/999,570
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent
; SEQ ID NO 1
; LENGTH: 2016
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1..1434
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1435..1836
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 1837..2016
; FEATURE:
; NAME/KEY: polyA_signal
; LOCATION: 1965..1970
; FEATURE:
; NAME/KEY: polyA_site
; LOCATION: 2001..2016
US-09-999-570-1

Query Match 40.5%; Score 485.2; DB 10; Length 2016;
Best Local Similarity 94.7%; Pred. No. 1.4e-132;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

Qy	73	TATTTAACTTTCTCTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT	132
Db	2012	TTTTTTTTTTCTCTCTCTGCTTGTCAAATGAGAGTTAGATTTATTTTACATTTGCT	1953
Qy	133	AAGTGCTCTGATCTGCTCATGAATCTTCTATGGGGAGAGCTGTGGGCGAGATTCCTTA	192
Db	1952	AAGTGCTCTGATCTGCTCATGAATCTTCTATGGGGAGAGCTGTGGGCGAGATTCCTTA	1893
Qy	193	AGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAITTCGCTACTTC	252
Db	1892	AGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAITTCGCTACTTC	1833
Qy	253	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGGTGGAGCCGCA	312
Db	1832	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGGTGGAGCCGCA	1773
Qy	313	ATTAGGAAAAGAGCTCTGGAAGCCACCTTGGCCATCTCTACACTGGTCCAGGTCCTTC	372
Db	1772	ATTAGGAAAAGAGCTCTGGAAGCCACCTTGGCCATCTCTACACTGGTCCAGGTCCTTC	1713
Qy	373	ATTATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAATCCTTT	432
Db	1712	ATTATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAATCCTTT	1653
Qy	433	TCCATGAGTACTCTCAGGTCCTCTTTGTTAAAGTAGCCTTTATCCCGAGCAATTTGTGA	492

1552	TCCATGAGTACTCTCAGGTCCTCTTGGTTAAGTAGCCTTTATCCCGACGAATTTGTGA	1593
Db		
493	AATGTAACATCATGTGTTTCCATCGCGTGTTTCCATTTTGAGATGCAATTTGGTGTGTGTC	552
Qy		
1592	AATGTAACATCATGTGTTTCCATCGCGTGTTTCCATTTTGAGATGCAATTTGGTGTGTGTC	1533
Db		
553	GTTGAAGCCTTTGGCGGAGGCGCGGACGCTGGGCGGAGCTTGGCGGAGCT	602
Qy		
1532	GTTGAAGCCACAGAGGCTCAGTGCAGAGTCTGGGCGGCAAGAAAAAGGT	1483
Db		

RESULT 25

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US-10-000-489-1/c
; Sequence 1, Application US/10000489
; Publication No. US2003092011A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; ATTORNEY: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CDNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US.6.DIV
; CURRENT APPLICATION NUMBER: US/10/000,489
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: US 09/924,340
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: JPatent

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Query Match	40.5%	Score	485.2	DB 14	Length	2016
Best Local Similarity	94.7%	Pred. No.	1.4e-132			
Matches	502	Conservative	0	Mismatches	28	Indels
					0	Gaps

Qy	73	TATTTAACTTTTCTTTCTCTGCTGTGCAAAATGAGAGGATTTAGATTTTATTTTTCACATTTGCT	132
Db	2012	TTTTTTTTTTTTTCTTTCTCTGCTGTGCAAAATGAGAGTTTAGATTTTATTTTTCATATTTGCT	1953
Qy	133	AAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGNAAGCTGTGGGGCAGATTCCTTA	192
Db	1952	AAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGAAAGCTGTGGGGCAGATTCCTTA	1893
Qy	193	AGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTTCATTTTCTGCCACTTTC	252
Db	1892	AGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGNACTGCTCATTTCTGCCACTTTC	1833
Qy	253	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTGCATGCAATGGTGAAGCCCGCA	312
Db	1832	TTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTGCATGCAATGGTGAAGCCCGCA	1773

Qy	313	ATTAGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC	312
Db	1772	ATTAGGAAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTC	1713
Qy	373	ATTATTTTGTCCACAGCCAGCAGGGTCTTTTGTGATTTTCCAAAAATCCAGGGAACCTCCTTT	432
Db	1712	ATTATTTTGTCCACAGCCAGCAGGGTCTTTTGTGATTTTCCAAAAATCCAGGGAACCTCCTTT	1653
Qy	433	TCCATGAGTACTCTCAGGTCCTCTTTGTGTAAGTAGCCTTTATCCCAAGCAATTTGTGA	492
Db	1652	TCCATGAGTACTCTCAGGTCCTCTTTGTGTAAGTAGCCTTTATCCCAAGCAATTTGTGA	1593
Qy	493	AATGTAAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCACTTTTGGTGTGGTCC	552
Db	1592	AATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCACTTTTGGTGTGGTCC	1533
Qy	553	GTTCGAAGCCTTGCCGAGCGCGCGACGCTGGGCGAGCTGGGCGAGCT	602
Db	1532	GTTCGAAGCACCAGAGGCTCAGTTCGAGGCTCTGGGCAGGCAAGAAAGGT	4483

RESULT 26

US-10-000-986-1/c
; Sequence 1, Application US/1000986
; Publication No. US20030096247A1
; GENERAL INFORMATION:
; APPLICANT: Benjanin, Stephane
; APPLICANT: Tanaka, Hiroaki
; TITLE OF INVENTION: HUMAN CNAS AND PROTEINS AND USES THEREOF
; FILE REFERENCE: 91.US9.DIV
; CURRENT APPLICATION NUMBER: US/10/000,986
; CURRENT FILING DATE: 2001-11-14
; PRIORITY APPLICATION NUMBER: US 09/924,340
; PRIORITY FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: PCT/IB01/01715
; PRIOR FILING DATE: 2001-08-06
; PRIOR APPLICATION NUMBER: US 60/305,456
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/302,277
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: US 60/298,698
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: US 60/293,574
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Jpatent

Query Match	40.5%	Score 485.2	DB 14	Length 2016
Best Local Similarity	94.7%	Pred. No. 1.4e-132		
Matches 502: Conservative	0	Mismatches 28	Indels 0	Gaps 0

Qy	73	TATTTAACTTTTCTTCTCTGCTGTGCAAAAGAGAGCTTAGATTTTATTTTACATTTGCT	132
Db	2012	TTTTTTTTTTTTCTTCTCTGCTGTGCAAAAGAGAGCTTAGATTTTATTTTACATTTGCT	1953
Qy	133	AACTGTCCTGATCTGCTCATGAATCTTTCTATGGGGGAAGCTGTGGGCGAGATTCCTTA	192


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; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46392
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-46392

Query Match          39.3%; Score 471.6; DB 17; Length 482;
Best Local Similarity 99.2%; Pred. No. 7.3e-129;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAACCTAAAGAAACCTTTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 478 GAACCTTAAAAAGAACTTTATTGAGGGCAAGGGGGTGCAAAACAATACAAAAATCAA 419

QY 61 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 120
Db 418 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 359

QY 121 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
Db 358 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 299

QY 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 240
Db 298 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 239

QY 241 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 300
Db 238 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 179

QY 301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 360
Db 178 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 119

QY 361 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 420
Db 118 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 59

QY 421 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 478
Db 58 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 1

RESULT 31
US-10-085-783A-46392/c
; Sequence 46392, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 46392
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-46392

Query Match          39.3%; Score 471.6; DB 17; Length 482;
Best Local Similarity 99.2%; Pred. No. 7.3e-129;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAACCTAAAGAAACCTTTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 478 GAACCTTAAAAAGAACTTTATTGAGGGCAAGGGGGTGCAAAACAATACAAAAATCAA 419

QY 61 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 120
Db 418 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 359

QY 121 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
Db 358 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 299

QY 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 240
Db 298 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 239

QY 241 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 300
Db 238 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 179

QY 301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 360
Db 178 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 119

QY 361 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 420
Db 118 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 59

QY 421 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 478
Db 58 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 1
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; SEQ ID NO 46392
; LENGTH: 482
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-46392

Query Match          39.3%; Score 471.6; DB 18; Length 482;
Best Local Similarity 99.2%; Pred. No. 7.3e-129;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGAACCTAAAGAAACCTTTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 478 GAACCTTAAAAAGAACTTTATTGAGGGCAAGGGGGTGCAAAACAATACAAAAATCAA 419

QY 61 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 120
Db 418 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 359

QY 121 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
Db 358 TTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 299

QY 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 240
Db 298 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAAT 239

QY 241 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 300
Db 238 TCTGCCCTACTCTTCTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCATTCGATGCAATG 179

QY 301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 360
Db 178 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 119

QY 361 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 420
Db 118 TCCAGGTCCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCCAAAAATCCA 59

QY 421 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 478
Db 58 GGGAACTCCCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTAAAGTAGCCTTTATCCC 1

RESULT 32
US-10-242-535A-57930/c
; Sequence 57930, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 57930
; LENGTH: 472
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-57930

Query Match          38.5%; Score 461.4; DB 17; Length 472;
Best Local Similarity 98.7%; Pred. No. 7.6e-126;
Matches 465; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
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Qy 303 GAGCGCCGAATAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTC 362
Db |||||||
Qy 180 GAGCGCCGAATAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTC 121
Db |||||||
Qy 363 CAGTCCTTCATTTATTTGTCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 422
Db |||||||
Qy 120 CAGTCCTTCATTTATTTGTCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 61
Db |||||||
Qy 423 GAATCTCTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCAGC 482
Db |||||||
Qy 60 GAATCTCTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCAGC 1

RESULT 35
US-10-085-783A-49122/c
; Sequence 49122, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 49122
; LENGTH: 480
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-49122

Query Match 37.4%; Score 448; DB 18; Length 480;
Best Local Similarity 95.8%; Pred. No. 7.2e-122;
Matches 460; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 3 AACTTAAAGAAAGACTTTATTTATTTAGGCGCAAGGGATGCAAAACAAATACAAAATCAAAA 62
Db |||||||
Qy 480 AACTTAAAGAAAGACTTTATTTATTTAGGCGCAAGGGATGCAAAACAAATACAAAATCAAAA 421
Db |||||||
Qy 63 GCTTATCTGGTATTTAACTTTTCTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTT 122
Db |||||||
Qy 420 GCTTATCTGGTATTTAACTTTTCTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTT 361
Db |||||||
Qy 123 TACATTTGCTAAAGTCTCTGATCTGCTCATGAATCTCTTATGCGGGGAAAGCTGTGGGC 182
Db |||||||
Qy 360 TACATTTGCTAAAGTCTCTGATCTGCTCATGAATCTCTTATGCGGGGAAAGCTGTGGGC 301
Db |||||||
Qy 183 AGATTCCTTAAGGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGCAACTGTCTCATTTTC 242
Db |||||||
Qy 300 AGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGCAACTGTCTCATTTTC 241
Db |||||||
Qy 243 TGCCTACTCTTCTTCCCTTCTGCTTCATGTGCTACAAAATAGTCAATGCAATGGT 302
Db |||||||
Qy 240 TGCCTACTCTTCTTCCCTTCTGCTTCATGTGCTACAAAATAGTCAATGCAATGGT 181
Db |||||||
Qy 303 GAGCGCCGAATAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTC 362
Db |||||||
Qy 180 GAGCGCCGAATAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTC 121
Db |||||||
Qy 363 CAGTCCTTCATTTATTTGTCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 422
Db |||||||
Qy 120 CAGTCCTTCATTTATTTGTCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 61
Db |||||||
Qy 423 GAATCTCTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCAGC 482
Db |||||||

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Db 60 GAATCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCAGC 1

RESULT 36
US-10-242-535A-56036/c
; Sequence 56036, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56036
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: n is a, c, g, or t
US-10-242-535A-56036

Query Match 37.2%; Score 446.4; DB 17; Length 474;
Best Local Similarity 98.9%; Pred. No. 2.1e-121;
Matches 469; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 9 AAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAAAT-ACAAAAATCAAAAGCTTA 67
Db |||||||
Qy 474 AAAAGAACTTTATTTATTTAGGCGCAAGGGATGCAAAACAAATCAAAAGCTTA 415
Db |||||||
Qy 68 TCTGGTATTTAACTTTTCTCTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACAT 127
Db |||||||
Qy 414 TCTGGTATTTAACTTTTCTCTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACAT 355
Db |||||||
Qy 128 TTGCTAAGTCTCTGATCTGCTCATGAATCTCTTCTATGCGGGAAGCTGTGGGCGAGATT 187
Db |||||||
Qy 354 TTGCTAAGTCTCTGATCTGCTCATGAATCTCTTCTATGCGGGAAGCTGTGGGCGAGATT 295
Db |||||||
Qy 188 CCTTAAGCGACCCCTTTTGGGACAACTCTTATCAGGAGGAGCGCAACTGCTCATTTTCTGCCT 247
Db |||||||
Qy 294 CCTTAAGCGACCCCTTTTGGGACAACTCTTATCAGGAGGAGCGCAACTGCTCATTTTCTGCCT 235
Db |||||||
Qy 248 ACTTCTTTCCCTTCTGCTTCATGTGCTACTACAAAATAGTCAATGCAATGGTGAGGC 307
Db |||||||
Qy 234 ACTTCTTTCCCTTCTGCTTCATGTGCTACTACAAAATAGTCAATGCAATGGTGAGGC 175
Db |||||||
Qy 308 CGCAATTAGGGAAGAAAGAGCTCTGGAAGCCACTTTGGCCATCTCTACACTGGTCCAGGT 367
Db |||||||
Qy 174 CGCAATTAGGGAAGAAAGAGCTCTGGAAGCCACTTTGGCCATCTCTACACTGGTCCAGGT 115
Db |||||||
Qy 368 CTTTCAATTTATTTGTCCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGGAACT 427
Db |||||||
Qy 114 CTTTCAATTTATTTGTCCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGGAACT 55
Db |||||||
Qy 428 CTTTTCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCA 480
Db |||||||
Qy 54 CTTTTCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCCCCA 1

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RESULT 37

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US/01-085-783A-56036/c
; Sequence 56036, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew C C.
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: patentIn version 3.2
; SEQ ID NO 56036
; LENGTH: 474
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (432)..(432)
; OTHER INFORMATION: n is a, c, g, or t
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (436)..(436)
; OTHER INFORMATION: n is a, c, g, or t
US-10-085-783A-56036

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Query Match	37.2%	Score	446.4	DB	18	Length	474
Best Local Similarity	98.9%	Pred. No.	2.le-121				
Matches	469	Conservative	0	Mismatches	3	Indels	2
Gaps	2						
Qy	9	AAAAGAACTTTATTTATTTAGGGGCAAGGGATGCAAAACAAT-ACAAAAATCAAAAGCTTA	67				
Db	474	AAAAGAACTTTATTTATTTAGGGGCAAGGGATGCAAAACNACNCAAAATCAAAAGCTTA	415				
Qy	68	TCTGGTATTAAACTTTTCTCTGCTGTGTCAAAATGAGAGTTAGATTTTATTTTTTACAT	127				
Db	414	TCTGGTATTAAACTTTTCTCTGCTGTGTCAAAATGAGAGTTAGATTTTATTTTTTACAT	355				
Qy	128	TTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGGCGACATT	187				
Db	354	TTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGGCGACATT	295				
Qy	188	CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGGGAACCTGCTCATTTCTGCCT	247				
Db	294	CCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGGGAACCTGCTCATTTCTGCCT	235				
Qy	248	ACTTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTCGATGCAATGTGAGGC	307				
Db	234	ACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTCGATGCAATGTGAGGC	175				
Qy	308	CCGCAATTAGGGAAGAAAGCTCTGGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT	367				
Db	174	CCGCAATTAGGGAAGAAAGCTCTGGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGT	115				
Qy	368	CCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCAGGGAAC	427				
Db	114	CCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCAGGGAAC	55				
Qy	428	CCTTTTCCATGAGTACTCTCAGTGCC-TCCTTTGTTAAGTAGCCTTTATATCCCA	480				
Db	54	CCTTTTCCATGAGTACTCTCAGTGCCCTTCTTTGTTAAGTAGCCTTTATATCCCA	1				

RESULT 38

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US-10-242-535A-56504/c
; Sequence 56504, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liew, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242.535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 56504
; LENGTH: 448
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-56504

Query Match          36.2%;   Score 434.4;   DB 17;   Length 448;
Best Local Similarity 99.6%;   Pred. No. 7.5e-118;
Matches 446;   Conservative 0;   Mismatches 1;   Indels 1;   Gaps

Qy      1  GGAACATAAAAGAACTTTATTATTGAGGCGAAGGGATGCAAAAC-AATACAAAAATCA
Db      448  GGAACATAAAAGAACTTTATTATTGAGGCGAAGGGATGCAAAACAAATAACAAAAATCA

Qy      60  AAAGCTTATCTGGTATTTAACTTTTCTCTGCTGTGCAAAATGAGAGTTAGATTTTAT
Db      388  AAAGCTTATCTGGTATTTAACTTTTCTCTGCTGTGCAAAATGAGAGTTAGATTTTAT

Qy      120  TTTTACATTTGCTAAGTCTGCTGATCTGCTCATGAAATCTCTATATGGGGAAGCTGTGG
Db      328  TTTTACATTTGCTAAGTCTGCTGATCTGCTCATGAAATCTCTATATGGGGAAGCTGTGG

Qy      180  GGCAGATTCCTTTAAGCGACCCCTTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT
Db      268  GGCAGATTCCTTTAAGCGACCCCTTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT

Qy      240  TTCTGCCTACTCTTTTCCCTTCTGCTTCATGTGTAACAAAATAGTCATTGCAATGCAAT
Db      208  TTCTGCCTACTCTTTTCCCTTCTGCTTCATGTGTAACAAAATAGTCATTGCAATGCAAT

Qy      300  GGTGAGGCCCGCAATTTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTTGCATCTCTACAGTG
Db      148  GGTGAGGCCCGCAATTTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTTGCATCTCTACAGTG

Qy      360  GTCCAGGTCCTTTCATTATTTTGTCCACAGCGAGGGTCTTTTGTGTTTTTCCAAAAATCC
Db      88  GTCCAGGTCCTTTCATTATTTTGTCCACAGCGAGGGTCTTTTGTGTTTTTCCAAAAATCC

Qy      420  AGGGAACCTCTTTTCCATGAGTACTCTC 447
Db      28  AGGGAACCTCTTTTCCATGAGTACTCTC 1

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RESULT 39
US-10-085-783A-56504/c
; Sequence 56504, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; APPLICANT: Liaw, C.C.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085-783A

QY 185 ATTCTTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAACTGCTCATTTCTG 244
DB 406 ATTCTTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGGAACTGCTCATTTCTG 347
QY 245 CCTACTCTTTCCCTTCCTCTGCTTCTGCTGCTACTGCTACAAATAGTCTCATTCGCAATGCTGA 304
DB 346 CCTACTCTTTCCCTTCCTCTGCTTCTGCTGCTACTGCTACAAATAGTCTCATTCGCAATGCTGA 287
QY 305 GCGCCGCAATTAGGGAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTCCA 364
DB 286 GCGCCGCAATTAGGGAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTCCA 227
QY 365 GGTCTCTCATTTATTTTGTGCCAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCAGGGA 424
DB 226 GGTCTCTCATTTATTTTGTGCCAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCAGGGA 167
QY 425 ACTCTCTTTCCATGAGTACTCTCAGGTCTCTCTGTTTAACTAGTCTTATCCCCAGGA 484
DB 166 ACTCTCTTTCCATGAGTACTCTCAGGTCTCTCTGTTTAACTAGTCTTATCCCCAGGA 107
QY 485 ATTTGTGAATGTAAACATCATGTGTTTCCATGGCGTGTTCCTATTTGAGATGGCATTTGG 544
DB 106 ATTTGTGAATGTAAACATCATGTGTTTCCATGGCGTGTTCCTATTTGAGATGGCATTTGG 47
QY 545 TG 546
DB 46 TG 45
RESULT 42
US-09-997-003-26/c
; Sequence 26, Application US/09997003
; Publication No. US20030203361A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PA003P1
; CURRENT APPLICATION NUMBER: US/09/997,003
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: unassigned
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: PCT/US00/22157
; PRIOR FILING DATE: 2000-08-11
; PRIOR APPLICATION NUMBER: 60/148,680
; PRIOR FILING DATE: 1999-08-13
; NUMBER OF SEQ ID NOS: 56
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 441
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-997-003-26
Query Match 34.3%; Score 411; DB 10; Length 441;
Best Local Similarity 100.0%; Pred.No. 6.4e-111;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGAAGCTAAAGAACTTTATTTATTTAGGCGAAGGGATGCAACAAATACAAAATCAA 60
DB 418 GGAAGCTAAAGAACTTTATTTATTTAGGCGAAGGGATGCAACAAATACAAAATCAA 359
QY 61 AAGCTTATCTGGTATTTAACTTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTTATT 120
DB 358 AAGCTTATCTGGTATTTAACTTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTTATT 299
QY 121 TTATCATTTGTAAGTGCTGATCTGCTATGATAATCCTTCTATGGGGGAAGCTGTGGG 180
DB 298 TTATCATTTGTAAGTGCTGATCTGCTATGATAATCCTTCTATGGGGGAAGCTGTGGG 239
QY 181 CGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGGAGGAGGCACTCTCATTT 240
DB 238 CGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGGAGGAGGCACTCTCATTT 179

QY 241 TCTGCGCTACTTCTTTTCCCTTCTGCTTCACTGTGTAATAAAAAATAGTCAATGCAATG 300
DB 178 TCTGCGCTACTTCTTTTCCCTTCTGCTTCACTGTGTAATAAAAAATAGTCAATGCAATG 119
QY 301 GTGAGGCGCCCAATTAGGGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
DB 118 GTGAGGCGCCCAATTAGGGAAGAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 59
QY 361 TCAGAGTCTCTTCATTTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCC 411
DB 58 TCAGAGTCTCTTCATTTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCC 8
RESULT 43
US-10-106-698-2418/c
; Sequence 2418, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA005P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: PatentIn Ver. 3.0
; SEQ ID NO 2418
; LENGTH: 632
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (7)..(7)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc_feature
; LOCATION: (24)..(24)
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; LOCATION: (40)..(40)
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; LOCATION: (593)..(593)
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; NAME/KEY: misc feature
; LOCATION: (595)..(595)
; OTHER INFORMATION: n equals a,t,g, or c
; NAME/KEY: misc feature
; LOCATION: (621)..(621)
; OTHER INFORMATION: n equals a,t,g, or c
US-10-106-698-2418

Query Match      33.0%; Score 396.2; DB 15; Length 632;
Best Local Similarity 95.7%; Pred. No. 1.9e-106;
Matches 424; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

Qy 1 GGAACATAAAAGAACTTTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 512 GGAACATAAAAGAACTTTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 453
Qy 61 AAGCTTATCTGGTATTAACTTTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 120
Db 452 AAGCTTATCTGGTATTAACTTTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 393
Qy 121 TTTCATTTTGGT--AAGTGTCTGAT--CTGCTCATGAAATCTTCTATGCGGAAGCTGT 177
Db 392 TTTCATTTGCTNAAGTGTCTGNTGNGTCCNTAANTCTTNTAAGGGNAAGTGT 333
Qy 178 GGGGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTC 237
Db 332 GGGGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTC 273
Qy 238 ATTTCTGCTACTTCTTTCCCTTCTGCTTATGATGTAATACAAAATAGTCAATGCA 297
Db 272 ATTTCTGCTACTTCTTTCCCTTCTGCTTATGATGTAATACAAAATAGTCAATGCA 213
Qy 298 ATGTGTAGGCGCCCAATTTAGGAAAGAAAGCTCTGGAAGCCCACTTTTGCCATCTCTAC 357
Db 212 ATGTGTAGGCGCCCAATTTAGGAAAGAAAGCTCTGGAAGCCCACTTTTGCCATCTCTAC 153
Qy 358 TGGTCCAGGTCCTTCATTATTGTCACAGCCAGAGGGTCTTTTGGATTTTCCAAAAAT 417
Db 152 TGGTCCAGGTCCTTCATTATTGTCACAGCCAGAGGGTCTTTTGGATTTTCCAAAAAT 93
Qy 418 CCAGGGAACCTCTTTTCATGAG 440
Db 92 CCAGGGAACCTCTTTTCATGAG 70

RESULT 44
US-10-242-535A-45565/c
; Sequence 45565, Application US/10242535A
; Publication No. US20040013663A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2005
; CURRENT APPLICATION NUMBER: US/10/242,535A
; CURRENT FILING DATE: 2002-09-12
; PRIOR APPLICATION NUMBER: US 10/085,783
; PRIOR FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; BEST LOCAL SIMILARITY 99.5%; PRED. NO. 5.5e-101;
; MATCHES 389; CONSERVATIVE 0; MISMATCHES 1; INDELS 1; GAPS 1;
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; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45565
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Human
US-10-242-535A-45565

Query Match      31.5%; Score 377.4; DB 17; Length 392;
Best Local Similarity 99.5%; Pred. No. 5.5e-101;
Matches 389; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 GGAACATAAAAGAACTTTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 391 GGAACATAAAAGAACTTTTATTGAGGCAAGGGGATGCAAAACAATACAAAAATCAA 332
Qy 61 AAGCTTATCTGGTATTAACTTTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 120
Db 331 AAGCTTATCTGGTATTAACTTTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 272
Qy 121 TTTCATTTTGGTAAAGTGTCTGATCTGATCAATGAAATCTTCTATGCGGAAGCTGT-GG 179
Db 271 TTTCATTTTGGTAAAGTGTCTGATCTGATCAATGAAATCTTCTATGCGGAAGCTGTGG 212
Qy 180 GCAGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCAT 239
Db 211 GCAGAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCAT 152
Qy 240 TTCTGCTACTTCTTTCCCTTCTGCTTCTGCTATGCTACTACAAAATAGTCAATGCAAT 299
Db 151 TTCTGCTACTTCTTTCCCTTCTGCTTCTGCTTCTGCTACTACAAAATAGTCAATGCAAT 92
Qy 300 GTTGAGGCGCGCAATTTAGGAAAGAAAGCTCTGGAAGCCCACTTTTGCCATCTCTACACTG 359
Db 91 GGTGAGGCGCGCAATTTAGGAAAGAAAGCTCTGGAAGCCCACTTTTGCCATCTCTACACTG 32
Qy 360 GTCCAGGTCCTTCATTATTGTCACAGCC 390
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RESULT 45
US-10-085-783A-45565/c
; Sequence 45565, Application US/10085783A
; Publication No. US20040037841A1
; GENERAL INFORMATION:
; APPLICANT: ChondroGene Inc.
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
; FILE REFERENCE: 4231/2002
; CURRENT APPLICATION NUMBER: US/10/085,783A
; CURRENT FILING DATE: 2002-02-28
; PRIOR APPLICATION NUMBER: US 60/305,340
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 60/275,017
; PRIOR FILING DATE: 2001-03-12
; PRIOR APPLICATION NUMBER: US 60/271,955
; PRIOR FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 58994
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 45565
; LENGTH: 392
; TYPE: DNA
; ORGANISM: Human
US-10-085-783A-45565

Query Match      31.5%; Score 377.4; DB 18; Length 392;
Best Local Similarity 99.5%; Pred. No. 5.5e-101;
Matches 389; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 22:33:12 ; Search time 5198 Seconds
(without alignments)
11176.953 Million cell updates/sec

Title: US-10-735-577-16
Perfect score: 1199
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Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_on.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pr.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	640.8	53.4	185447	9	AL450992 Human DNA
2	638	53.2	638	6	CQ715898 Sequence
3	637.8	53.2	673	9	BC015973 Homo sapi
4	601	50.1	649	6	CQ878718 Sequence
5	601	50.1	649	6	AR489221 Sequence
6	601	50.1	649	6	AX409703 Sequence
7	601	50.1	649	6	AX710164 Sequence
8	601	50.1	649	6	AX779835 Sequence
9	601	50.1	649	9	HUMCLANNII
10	598	49.9	609	9	M81457 Human calpa
11	557	46.5	579	6	AR489209 Sequence
12	537	44.8	571	6	AX396675 Sequence
13	530	44.2	642	9	AX179865 Macaca mu
14	523	43.6	582	6	AX899035 Sequence
15	523	43.6	582	6	B0034568 Sequence
16	516	43.0	538	6	CQ702692 Sequence
17	485.2	40.5	2016	6	AX616317 Sequence
18	471.6	39.3	482	6	CQ701466 Sequence
19	461.4	38.5	472	6	CQ713004 Sequence

C 20	448	37.4	480	6	CQ704196
C 21	446.4	37.2	474	6	CQ711110
C 22	434.4	36.2	448	6	CQ711578
C 23	434	36.2	604	4	BOVCALPI
C 24	423	35.3	434	6	AX777886
C 25	389.2	32.5	480	9	HUMPL1A
C 26	377.4	31.5	392	6	CQ700639
C 27	374.2	31.2	534	4	AB098817
C 28	363.6	30.3	384	6	CQ709131
C 29	348.8	29.1	604	10	BC025044
C 30	344.8	28.8	365	6	CQ706246
C 31	343.6	28.7	600	6	AX306168
C 32	343.6	28.7	600	10	MUSCALPI
C 33	343	28.6	407	6	CQ711127
C 34	337.4	28.1	339	6	CQ671113
C 35	330.8	27.6	164679	9	AC005921
C 36	330	27.5	330	6	CQ711784
C 37	329.8	27.5	600	6	BD251901
C 38	329.8	27.5	600	6	AR202142
C 39	329.8	27.5	600	6	AR473726
C 40	329.8	27.5	600	6	AX407293
C 41	329.2	27.5	573	6	AX401698
C 42	329.2	27.5	573	6	AX710160
C 43	329.2	27.5	573	10	RATS100RP
C 44	328.4	27.4	570	6	AR489208
C 45	317	26.4	318	6	AX260435

ALIGNMENTS

RESULT 1

AL450992

LOCUS

DEFINITION

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

AL450992 Human DNA sequence from clone RP11-139D23 on chromosome 1, complete sequence.

AL450992 AC024491

AL450992.17 GI:18375805

HTG.

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 185447)

Martin, S.

Direct Submission

Submitted (18-JAN-2002) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk

On Jan 25, 2002 this sequence version replaced gi:16116488.

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations

together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping Group. Further information can be found at

http://www.sanger.ac.uk/HGP/Chr1

RP11-139D23 is from the library RPI-11.1 constructed by the group

of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
This sequence is the entire insert of clone Rp11-139D23 The true
left end of clone Rp11-353M1 is at 85124 in this sequence. The true
right end of clone Rp11-99D18 is at 22235 in this sequence.

FEATURES

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/db_xref="taxon:9606"
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/clone="Rp11-139D23"
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digest data confirm the assembly."

ORIGIN

Query Match 53.4%; Score 640.8; DB 9; Length 185447;
Best Local Similarity 97.5%; Pred. No. 7.3e-126;
Matches 651; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
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DB 154709 GAGGGGCGCTGGCGCGGCGGAGCTCACCTTGGCCGAGCGCGGCGAGCGTGGCGAG 154768
QY 592 CTGGCGAGCTGGAACGCGGCGGCGAGAGCGGCGGCGGCTGTGCGCCTTCCTTAGT 651
DB 154769 CTGGCGAGCTGGACGCGGCGGCGAGAGCGGCGGCGGCTGTGCGCCTTCCTTAGT 154828
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LOCUS CQ715898/c 638 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 1832 from Patent WO02068579.
ACCESSION CQ715898
VERSION CQ715898.1 GI:42276755
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Venter, C.J., Adams, M.C., Li, P.W. and Myers, E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of
humanexons or transcripts, for detecting expression and other uses
thereof
JOURNAL Patent: WO 02068579-A 1832 06-SEP-2002;
PE Corporation (NY) (US)
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Best Local Similarity 100.0%; Pred. No. 1.5e-125;
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RESULT 3
BC015973/c
LOCUS
DEFINITION
  Homo sapiens S100 calcium binding protein A10 (annexin II ligand,
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  IMAGE:4103596), complete cds.
ACCESSION
  BC015973
VERSION
  BC015973.1 GI:16359017
KEYWORDS
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SOURCE
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ORGANISM
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  1 (bases 1 to 673)
REFERENCE
  Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
  Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
  Altschul,S.F., Zeeberg,B., Buotow,K.H., Schaefer,C.F., Bhat,N.K.,
  Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
  Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
  Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
  Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
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  Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
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  Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
  Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
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  Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  Generation and initial analysis of more than 15,000 full-length
  human and mouse cDNA sequences
  Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
  12477932
  2 (bases 1 to 673)
  Strausberg,R.
  Direct Submission
  Submitted (22-OCT-2001) National Institutes of Health, Mammalian
  Gene Collection (MGC), Cancer Genomics Office, National Cancer
  Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
  USA
  NIH-MGC Project URL: http://mgc.nci.nih.gov
  Contact: MGC help desk
  Email: cgabbs-remail.nih.gov
  Tissue Procurement: ATCC
  cDNA Library Preparation: CLONTECH Laboratories, Inc.
  cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Institute for Systems Biology
  http://www.systemsbioology.org
  contact: amadanesystemsbiology.org
  Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha
  Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

  Clone distribution: MGC clone distribution information can be found
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RESULT 4
CQ878718/c

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LOCUS CQ878718 649 bp DNA linear PAT 04-OCT-2004
DEFINITION Sequence 3 from Patent WO2004080424.
ACCESSION CQ878718
VERSION CQ878718.1 GI:53791165
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Yeh, L.A., Cuny, G.D., Padmanaban, D. and Ding, K.
TITLE Methods and compositions for neurite outgrowth detection
JOURNAL Patent: WO 2004080424-A 3 23-SEP-2004;
THE BRIGHAM AND WOMEN'S HOSPITAL, INC. (US)
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ORIGIN
Query Match 50.1%; Score 601; DB 6; Length 649;
Best Local Similarity 99.7%; Pred. No. 1.2e-117;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
QY 1 GGAACATAAAAGAACTTTATTATTGAGGCGAAGGGATGCAAAACAATACAAAATCAA 60
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LOCUS AR489221/c
DEFINITION AR489221
ACCESSION AR489221
VERSION AR489221.1 GI:47256166
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 649)
AUTHORS Stanton, L.W., White, R.T., Damm, D.L., Lewicki, J.A., Joly, A. and Schreiner, G.F.
TITLE Methods for detection and use of differentially expressed genes in disease states
JOURNAL Patent: US 6709855-A 36 23-MAR-2004;
FEATURES
source Location/Qualifiers
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ORIGIN
Query Match 50.1%; Score 601; DB 6; Length 649;
Best Local Similarity 99.7%; Pred. No. 1.2e-117;
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QY 1 GGAACATAAAAGAACTTTATTATTGAGGCGAAGGGATGCAAAACAATACAAAATCAA 60
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RESULT 6
AX409703/c
LOCUS AX409703 649 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 2350 from Patent WO0229103.
ACCESSION AX409703
VERSION AX409703.1 GI:21442408
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1
REFERENCE
AUTHORS Alvares, C., Horne, D., Peres-da-Silva, S. and Vockley, J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 2350 11-APR-2002;
GENE LOGIC INC (US)
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ORIGIN
Query Match 50.1%; Score 601; DB 6; Length 649;
Best Local Similarity 99.7%; Pred. No. 1.2e-117;
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RESULT 7
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LOCUS AX710164 649 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 7 from Patent WO03016917.
ACCESSION AX710164
VERSION AX710164.1 GI:29786759
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
1
REFERENCE
AUTHORS Okuse, K., Baker, M., Poon, L., Wood, J.N. and Malik-Hall, M.
TITLE Sodium channel regulators and modulators
JOURNAL Patent: WO 03016917-A 7 27-FEB-2003;
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Best Local Similarity 99.7%; Pred. No. 1.2e-117;
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Db 170 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAATT 111
Qy 541 TTGCTGTGGTCCGTTGAAGCCTTGGCCGAGCGCGGAGCGCTGGCGAGCTGGCGAG 600

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RESULT 8
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LOCUS AX779835 649 bp DNA linear PAT 14-JUL-2003
DEFINITION Sequence 1992 from Patent WO03039443.
ACCESSION AX779835
VERSION AX779835.1 GI:32696829
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Haferlach,T., Schoch,C., Kern,W., Kohlmann,A., Schnittger,S.,
Dugas,M., Ellis,R., Brors,B. and Mergenthaler,S.
TITLE Novel genetic markers for leukemias
JOURNAL Patent: WO 03039443-A 1992 15-MAY-2003;
Deutsches Krebsforschungszentrum (DE);
Ludwig-Maximilian-Universitaet Muenchen (DE);
PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)
FEATURES
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ORIGIN
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Best Local Similarity 99.7%; Pred. No. 1.2e-117;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 GGAACATAAAAGAACTTTATTATTCAGGCGGAGGGATGCAACAATACAAATCAA 60
Db 649 GGAACATAAAAGAACTTTATTATTCAGGCGGAGGGATGCAACAATACAAATCAA 590
Qy 61 AAGCTTATCTGGTATTAACTTTTCTCTGCTGTCCTCAATCAGAGTTAGATTTATT 120
Db 589 AAGCTTATCTGGTATTAACTTTTCTCTGCTGTCCTCAATCAGAGTTAGATTTATT 530
Qy 121 TTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCCTTCTATGGGGGAAGCTGTGG 180
Db 529 TTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCCTTCTATGGGGGAAGCTGTGG 470
Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACCTCTATCAGGAGGAGCGAAGCTGCATT 240
Db 469 GCAGATTCCTTAAGCGACCCCTTTT-GGACAACCTCTATCAGGAGGAGCGAAGCTGCATT 411
Qy 241 TCTGCCCTACTCTTTCCCTTCTGCTTCATGCTGTAACAAAATAGTCATTCGATGCAATG 300
Db 410 TCTGCCCTACTCTTTCCCTTCTGCTTCATGCTGTAACAAAATAGTCATTCGATGCAATG 351
Qy 301 GTGAGGCCGCCAATTAGGGAAGAAAGAGCTGTGAAGCCCACTTTGCCATCTTACACTGG 360
Db 350 GTGAGGCCGCCAATTAGGGAAGAAAGAGCTGTGAAGCCCACTTTGCCATCTTACACTGG 291
Qy 361 TCCAGGTCCCTTCAATTATTATTGTCACAGCCAGAGGCTTTTGTGATTTTCCAAATCCA 420
Db 290 TCCAGGTCCCTTCAATTATTATTGTCACAGCCAGAGGCTTTTGTGATTTTCCAAATCCA 231
Qy 421 GGAACATCCCTTTTCCATGAGTACTCTCAGGCTCCTCTCTTTGTTAAGTAGCCCTTTATCCCCA 480
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Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 540
Db 170 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 111
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Qy 541 TTGGTGTGTCCTTGAAGCCTTGGCCGAGCGCGGACGCTGGCGAGCTGGCGGAG 600
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Qy 601 CTGGACCGCGGCGGAGCGGAGCGGAGC 625
Db 51 CTGGACCGCGGCGGAGCGGAGCGGAGC 27

RESULT 9
HUMCLANNII/c
LOCUS HUMCLANNII 649 bp mRNA linear PRI 31-DEC-1994
DEFINITION Homo sapiens cellular ligand of annexin II (p11) mRNA, complete
cds.
ACCESSION M38591
VERSION M38591.1 GI:180595
KEYWORDS cellular ligand of annexin II.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Kube,E., Weber,K. and Gerke,V.
TITLE Primary structure of human, chicken, and Xenopus laevis p11, a
cellular ligand of the Src-kinase substrate, annexin II
JOURNAL Gene 102 (2), 255-259 (1991)
MEDLINE 91340161
PUBMED 1831433
COMMENT Original source text: Homo sapiens (tissue library: lambda-GT10)
adenocarcinoma cDNA to mRNA.
Draft entry and computer-readable sequence for [Unpublished (1990)]
kindly submitted
by V.Gerke, 17-SEP-1990.
Max-Planck-Institute for Biophysical Chemistry
Dept Biochemistry
Am Fassberg
D-3400 Goettingen, FRG.
FEATURES
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112..405
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ORIGIN
Query Match 50.1%; Score 601; DB 9; Length 649;
Best Local Similarity 99.7%; Pred. No. 1.2e-117;
Matches 623; Conservative 0; Mismatches 0; Indels 2; Gaps 2;

Qy 1 GGAACATAAAAGAACTTTATTATTCAGGCGGAGGGATGCAACAATACAAATCAA 60
Db 649 GGAACATAAAAGAACTTTATTATTCAGGCGGAGGGATGCAACAATACAAATCAA 590
Qy 61 AAGCTTATCTGGTATTAACTTTTCTCTGCTTGTCAATGAGAGTTAGATTTATT 120
Db 589 AAGCTTATCTGGTATTAACTTTTCTCTGCTTGTCAATGAGAGTTAGATTTATT 530
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Qy	121	TTTACATTTGCTAAGTGTCCGTGATCTGCTCATGAAATCCTTCTATATGGGGGAAGCTGTGGG	180
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Qy	181	GCAGATTCCTTTAAGCGACCCCTTTTGGGCAACACTCTTTATCAGGGAGGAGCGAACTGCTCATTT	240
Db	469	GCAGATTCCTTTAAGCGACCCCTTT-GGACAACTCTTTATCAGGGAGGAGCGAACTGCTCATTT	411
Qy	241	TCTGCCCTACTCTTTTCCCTCTCTGCTTCAATGTACTACAAATAGTCAATTCATGCAATG	300
Db	410	TCTGCCCTACTCTTTTCCCTCTCTGCTTCAATGTACTACAAATAGTCAATTCATGCAATG	351
Qy	301	GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAAGCCCACTTTGCCATCTCTACACTGG	360
Db	350	GTGAGGCCCGCAATTAGGGAAAAGAGCTCTGGAAAGCCCACTTTGCCATCTCTACACTGG	291
Qy	361	TCCAGGTCTCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCA	420
Db	290	TCCAGGTCTCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCA	231
Qy	421	GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCCTTTGTATTAAGTACGCTTTATCCCA	480
Db	230	GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTCCTTTGTATTAAGTACGCTTTATCCCA	171
Qy	481	GCGAATTTGCAATGTAAACATCATGTGTTTCCATGGCGTGTTCATTTTGATATGGCAATT	540
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Qy	541	TTGTGTGTGTCCTGTGAAGCCTTTGGCCGAGGCGCGCGGAGCGCTGGGCGAGCTGGGCGAG	600
Db	110	TTGTGTGTGTCCTGTGAAGCCTTGG-CGAGGCGCGCGGAGCGCTGGGCGAGCTGGGCGAG	52
Qy	601	CTGAGCGCGGGCGGAGAGGCGAGC	625
Db	51	CTGAGCGCGGGCGGAGAGGCGAGC	27

RESULT 10	HUMCALPAIL/c
LOCUS	HUMCALPAIL
DEFINITION	Human calpactin I light chain mRNA, complete cds.
ACCESSION	M81457
VERSION	M81457.1 GI:179874
KEYWORDS	calpactin I light chain.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 609)
AUTHORS	Dooley,T.P., Weiland,K.L. and Simon,M.
TITLE	cDNA sequence of human p11 calpactin I light chain
JOURNAL	Genomics 13 (3), 866-868 (1992)
MEDLINE	92347895
PUBMED	1386341
COMMENT	Original source text: Homo sapiens (tissue library: lambda gt11) cDNA to mRNA.

REFERENCE
AUTHORS Stanton, L.W., White, R.T., Damm, D.L., Lewicki, J.A., Joly, A. and Schreiner, G.F.
TITLE Methods for detection and use of differentially expressed genes in disease states
JOURNAL Patent: US 6709855-A 24 23-MAR-2004;
FEATURES Location/Qualifiers
source 1..579
unclassified:
 1. (bases 1 to 579)

RESULT	11
AR489209/c	
LOCUS	AR489209
DEFINITION	Sequence 24 from patent US 6709855.
ACCESSION	AR489209
VERSION	AR489209.1 GI:47256154
KEYWORDS	.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 579) Scanlon,D.W., White,R.T., Damm,D.L., Lewicki,J.A., Joly,A. and Schreiner,G.F. Methods for detection and use of differentially expressed genes in disease states Patent: US 6709855-A 24 23-MAR-2004; Location/Qualifiers 1..579
TITLE	
JOURNAL	
FEATURES	

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ORIGIN

Query Match 46.5%; Score 557; DB 6; Length 579;
Best Local Similarity 99.7%; Pred. No. 2.9e-108;
Matches 579; Conservative 0; Mismatches 0; Indels 2; Gaps 2;
1 GGAACATAAAAGAACCTTTATTTATGAGGCGAAGGGATGCAACAAATACAAATCAAAATCAA 60
Db GGAACATAAAAGAACCTTTATTTATGAGGCGAAGGGATGCAACAAATACAAATCAAAATCAA 579
QY 61 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 120
Db AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 460
QY 121 TTATACATTTGCTAAGTCTCTGATCTCTCATGAAATCTTATCAGGAGGAGCGAAGCTGTGG 180
Db TTTACATTTGCTAAGTCTCTGATCTCTCATGAAATCTTATCAGGAGGAGCGAAGCTGTGG 400
QY 181 GCAGATTCCTTAAGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGAAGCTGTCTCA 240
Db GCAGATTCCTTAAGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGAAGCTGTCTCA 341
QY 241 TCTGCTTACTTCTTCCCTTCTGCTTCTCATGTGTAACAATAAGTCAATTCATGCAATG 300
Db TCTGCTTACTTCTTCCCTTCTGCTTCTCATGTGTAACAATAAGTCAATTCATGCAATG 281
QY 301 GTGAGGCGCGAATTAGGGAAGAAAGCTCTGAGAGCCCACTTTGCCATCTCTACACTGG 360
Db GTGAGGCGCGAATTAGGGAAGAAAGCTCTGAGAGCCCACTTTGCCATCTCTACACTGG 221
QY 361 TCAGAGTCTCTTCAATTTATTTGTCACAGCAGAGGCTTTTGTGATTTCCAAATAATCCA 420
Db TCAGAGTCTCTTCAATTTATTTGTCACAGCAGAGGCTTTTGTGATTTCCAAATAATCCA 161
QY 421 GGGAACTCTCTTCCATGAGTACTCTCAGGTCTCTCTCTTGTAAAGTAGCCCTTTATCCCCA 480
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QY 481 CGCAATTTGTGAATGTAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 540
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QY 541 TTGCTGTGTCCTGTTGAAGCTTGGCGAGCGCGCGGCGAC 581
Db TTGCTGTGTCCTGTTGAAGCTTGG-CGAGCGCGCGCGGAC 1

RESULT 12
AX396675
LOCUS AX396675
DEFINITION Sequence 890 from Patent WO0212328.
ACCESSION AX396675
VERSION AX396675.1 GI:21067422
KEYWORDS Homo sapiens (human)
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
AUTHORS King, G.E., Meagher, M.J., Xu, J. and Secrist, H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer
JOURNAL Patent: WO 0212328-A 890 14-FEB-2002;
CORIXA CORPORATION (US)
FEATURES
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ORIGIN

Query Match 44.8%; Score 537; DB 6; Length 571;
Best Local Similarity 98.7%; Pred. No. 5.2e-104;
Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
1 GGAACATAAAAGAACCTTTATTTATGAGGCGAAGGGATGCAACAAATACAAATCAAAATCAA 60
Db GGAACATAAAAGAACCTTTATTTATGAGGCGAAGGGATGCAACAAATACAAATCAAAATCAA 87
QY 61 AAGCTTATCTGGTATTTAACTTTTCTCTGCTTCTCAAAATGAGAGTTAGATTTTATT 120
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QY 121 TTATACATTTGCTAAGTCTCTGATCTCTCATGAAATCTTATCAGGAGGAGCGAAGCTGTGG 180
Db TTATACATTTGCTAAGTCTCTGATCTCTCATGAAATCTTATCAGGAGGAGCGAAGCTGTGG 207
QY 181 GCAGATTCCTTAAGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGAAGCTGTCTCA 240
Db GCAGATTCCTTAAGCGACCTTTTGGGACAACTCTTATCAGGAGGAGCGAAGCTGTCTCA 267
QY 241 TCTGCTTACTTCTTCCCTTCTGCTTCTCATGTGTAACAATAAGTCAATTCATGCAATG 300
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QY 421 GGGAACTCTCTTCCATGAGTACTCTCAGGTCTCTCTCTTGTAAAGTAGCCCTTTATCCCCA 480
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QY 541 TTGG 544
Db TTGG 571

RESULT 13
AY179865/c
LOCUS AY179865
DEFINITION Macaca mulatta S100 calcium binding protein A10 (S100A10) mRNA, complete cds.
ACCESSION AY179865.1 GI:27802540
VERSION AY179865
KEYWORDS Macaca mulatta (rhesus monkey)
SOURCE
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
Cercopitheciinae; Macaca.
REFERENCE 1 (bases 1 to 646)
AUTHORS Sun, X.-Y., Tan, Y.-F., Qin, L., Bai, S.-X., Li, F.-X., Qiu, W., Piao, Y.-S. and Wang, Y.-L.
TITLE Molecular cloning of genes critical to embryo implantation from Rhesus monkey by suppression subtractive hybridization
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 646)
AUTHORS Sun, X.-Y., Tan, Y.-F., Qin, L., Bai, S.-X., Li, F.-X., Qiu, W., Piao, Y.-S. and Wang, Y.-L.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2002) State Key Laboratory of Reproductive Biology, Institute of Zoology, Chinese Academy of Science, Bei Si Huan Xi Lu, #25, Hai Dian District, Beijing 100080, China
FEATURES
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Query Match 44.2%; Score 530; DB 9; Length 646;
Best Local Similarity 96.4%; Pred. No. 1.7e-102;
Matches 542; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db 617 GGAACCTAAAGAACTTTATTATTGAGGCAAGGGGATGCAAAACAATCAAAAAATCAA 558
Qy 61 AAGCTTATCTGGTATTAACTTTTCTCTCTGCTTGTCAATCAGAGTTAGATTTATT 120
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Qy 121 TTTACATTTGTAAGTGCTGATCTGCTCATGAAATCCTTCTATGGGGAGCTGTGGG 180
Db 497 TTTACATTTGTAAGTGCTGATCTGCTCATGAAATCCTTCTATGGGGAGCTGTGGG 438
Qy 181 CGAATTCCTTAAGACCCCTTTGGGACACTTTATCAGGAGGAGCGAACTGCTCAAT 240
Db 437 CGAATTCCTTAAGACCCCTTTGGGACAGCTTGTTCAGGAGGAGCGAACTGCTCGT 378
Qy 241 TCTGCCTACTTCTTCCCTCTGCTTCATGCTGTAATGTAATGTAATGTAATGTAATG 300
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Qy 301 GTGAGGCGCCCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 317 GTGAGGCGCCCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTGCACTGG 258
Qy 361 TCCAGGTCCTTCATATTGTCACAGCCAGAGGGTCTTTTGAATTTCAAAAAATCCA 420
Db 257 TCCAGGTCCTTCATATTGTCACAGCCAGAGGGTCTTTTGAATTTCAAAAAATCCA 198
Qy 421 GGGAACTCTTTCCATGAGTACTCTCAGGTCCTCTCTTGTGTAAGTAGCCCTTTATCCCCA 480
Db 197 GGAAGTCTCTTTCCATGAGTACTCTCAGGTCCTCTCTTGTGTAAGTAGCCCTTTATCCCCC 138
Qy 481 GCGAATTTGTGAATGTAACATCATGTTTCCATGGGCTGTTCCATTTGAGATGGCATT 540
Db 137 GCGAATTTGTGAATGTAACATCATGTTTCCATGGGCTGTTCCATTTGAGACGGCATT 78
Qy 541 TTGGTGTGGTCCGTTGAAGCCT 562
Db 77 TTGGTGTGGTCTGTTGAAGCTT 56

RESULT 14
AX899035/c
LOCUS BD034568/c
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034568
VERSION BD034568.1 GI:22576310
KEYWORDS JP 2001269182-A/10814.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Dumas Milne Edwards, J.B., Duclert, A. and Giordano, J.Y.
AUTHORS

TITLE Expressed sequence tags and encoded human proteins
JOURNAL Patent: EP 1033401-A 14898 06-SEP-2000;
Genet (FR)
FEATURES
source 1. 582
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/db_xref="taxon:9606"
ORIGIN
Query Match 43.6%; Score 523; DB 6; Length 582;
Best Local Similarity 97.9%; Pred. No. 5.1e-101;
Matches 547; Conservative 4; Mismatches 4; Indels 4; Gaps 2;
Qy 30 GGCAAGGGGATGCAAAACAATCAAAAAATCAAAAGCTTATCTGCTGATTTAACTTTCTTC 89
Db 582 GGCAAGGGGATGCAAAACAATCAAAAAATCAAAAGCTTATCTGCTGATTTAACTTTCTTC 523
Qy 90 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTTGTCTAAGTGTCTGATCTGCT 149
Db 522 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTTGTCTAAGTGTCTGATCTGCT 463
Qy 150 CATGAATTCCTTCTATGGGGAGAGCTGTGGGGAGAGTTCTTTAAGCGACCTTTTGGGACA 209
Db 462 CATGAATTCCTTCTATGGGGAGAGCTGTGGGGAGAGTTCTTTAAGCGACCTTTTGGGACA 405
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Db 404 ACTCTTATCAGGAGGAGCGAACTGCTCACTTCTGCTACTTCTTTCCCTTCTGCTTTCAT 345
Qy 270 GTGTACTAATAATAGTCAATGATGCAATGCTGAGGCGCCGCAATTTAGGGAAGAAAGCT 329
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Db 284 CTGGAAGCCCACTTGGCACTCTACACTGCTCCAGGCTCTCATTTATTTTGTCCACAGC 225
Qy 390 CAGAGGCTCTTTTGAATTTTCCAAATCCAGGAACTCTTTTCCAAGTACTCTCAG 449
Db 224 CAGAGGCTCTTTTGAATTTTCCAAATCCAGGAACTCTTTTCCAAGTACTCTCAG 167
Qy 450 GTCTCTCTTTGTAAGTAGCTTTATCCAGGCAATTTGTGAATGTAACATCATGCT 509
Db 166 GTCTCTCTTTGTAAGTAGCTTTATYCCAGGCAATTTGTGAATGTAACATCATGCT 107
Qy 510 TTCCATGGGCTGTTTCCATTTGAGATGCAATTTTGGTGTGCTCGTTTGAAGCTTTGGCCGA 569
Db 106 TTCCATGGGCTGTTTCCATTTGAGATGCAATTTTGGTGTGCTCGTTTGAAGCTTTGGCCGA 47
Qy 570 GGCGCGCGGAGCGCTGGGC 588
Db 46 GGCGCGCGGAGCGCTGGGC 28

RESULT 15
BD034568/c
LOCUS BD034568
DEFINITION Sequence tag and encoded human protein.
ACCESSION BD034568
VERSION BD034568.1 GI:22576310
KEYWORDS JP 2001269182-A/10814.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 582)
AUTHORS Edwards, J.B.D.M., Duclair, E. and Jordan, J.Y.
TITLE Sequence tag and encoded human protein
JOURNAL Patent: JP 2001269182-A 10814 02-OCT-2001;
COMMENT OS Homo sapiens (human)
PN JP 2001269182-A/10814

PD 02-OCT-2001
PF 24-FEB-2000 JP 2000118773
PR 26-FEB-1999 US 60/122487
PI JEAN BAPTISTE DUMAS MILNE EDWARDS, EIMERIC DUCCLAIR, JEAN YVES
PC C12N15/09, C07K14/435, C07K16/18, C12N1/15, C12N1/19, C12N1/21, PC
C12N5/10,
PC C12P21/02, C12P21/08, C12Q1/68, G06F17/30, C12N15/00, C12N5/00, PC
G06F15/40
CC
FH Key Location/Qualifiers.
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ORIGIN
Query Match 43.6%; Score 523; DB 6; Length 582;
Best Local Similarity 97.9%; Pred. No. 5.1e-101;
Matches 547; Conservative 4; Mismatches 4; Indels 4; Gaps 2;
Qy 30 GCGAAGGGATGCAAAACATACAAATCAAAAGCTTATCTGTATTTAACTTTCTTTC 89
Db 582 GCGAAGGGATGCAAAACATACAAATCAAAAGCTTATCTGTATTTAACTTTCTTTC 523
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Qy 150 CATGAATTCCTTCTATGGGGAGAGCTGTGGGCGAGATTCCTTAAGCGACCTTTTGGGACA 209
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Qy 210 ACTCTTATCAGGGAGGAGCGAATCTGCTCATTTCTGCTTCTTCTTCTTCTTCTGCTTCAT 269
Db 404 ACTCTTATCAGGGAGGAGCGAATCTGCTCATTTCTGCTTCTTCTTCTTCTTCTTCTTCT 345
Qy 270 GTGTACTACAAATAGTTCATTGATGCAATGCTGAGCGCCGCAATAGGGAAGAAAGAGCT 329
Db 344 GTGTACTACAAATAGTTCATTGATGCAATGCTGAGCGCCGCAATAGGGAAGAAAGAGCT 285
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Db 284 CTGGAAGCCACCTTTGCCATCTCTACATGCTGCTCAGGTCCTTCTCATTTTGTCCACAGC 225
Qy 390 CAGAGGTCCTTTTGAATTTCCAAATCAGGGAATCTCTTCCATGAGTACTCTCAG 449
Db 224 CAGAGGTCCTTTTGAATTTCCAAATCAGGGAATCTCTTCCATGAGTACTCTCAG 167
Qy 450 GTCTCTCTTTGTTAAGTAGCTTTTATCCCGAGCGAATTTGTGAATGTAACATCATGCT 509
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Qy 510 TTCCATGCGGTGTTCCATTTGAGATGCGATTTTGGTGTGTCGTTGAAGCCTTTGGCCGA 569
Db 106 TTCCATGCGGTGTTCCATTTGAGATGCGATTTTGGTGTGTCGTTGAAGCCTTTGGCCGA 47
Qy 570 GCGCGGCGGAGCGTGGGC 588
Db 46 GCGCGGCGGAGCTGTGCGC 28

REFERENCE 1
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 47618 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1. .538
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Query Match 43.0%; Score 516; DB 6; Length 538;
Best Local Similarity 98.9%; Pred. No. 1.6e-99;
Matches 530; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 8 AAAAAAAGCTTTATTTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAAAAGCTTA 67
Db 535 AAAAAAGACCTTTATTTATTGAGGGCAAGGGGATGCAAAACAATCAAAATCAAAAGCTTA 476
Qy 68 TCTGCTATTAACTTTTCTTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTTACAT 127
Db 475 TCTGCTATTAACTTTTCTTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTTTACAT 416
Qy 128 TTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 187
Db 415 TTGCTAAGTGCTCTGATCTGCTCATGAATCCTTCTATGGGGGAAGCTGTGGGGCAGATT 356
Qy 188 CTTAAAGCAAGCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTCTCATTTCTGCCT 247
Db 355 CTTAAAGCAAGCTTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTCTCATTTCTGCCT 296
Qy 248 ACTTCTTCCCTTCTGCTTCTGCTGCTACTACAAAATAGTTCATGCAATGCAATGCTGAGGC 307
Db 295 ACTTCTTCCCTTCTGCTTCTGCTGCTACTACAAAATAGTTCATGCAATGCAATGCTGAGGC 236
Qy 308 CCGCAATTAGGGAAAAAGAGCTCTGGAAGCCCACTTTTGGCATCTCTACACTTGTCTCCAGGT 367
Db 235 CCGCAATTAGGGAAAAAGAGCTCTGGAAGCCCACTTTTGGCATCTCTACACTTGTCTCCAGGT 176
Qy 368 CTTTCATTTTGTCCACAGCGAGGCTCTTTTGTATTTTCCAAAAATCCAGGGAAT 427
Db 175 CTTTCATTTTGTCCACAGCGAGGCTCTTTTGTATTTTCCAAAAATCCAGGGAAT 116
Qy 428 CTTTTCATGAGTACTCTCAGGCTCTCTTCTGCTTAAAGTAGCTTTATCCCGAGCGAAT 487
Db 115 CTTTTCATGAGTACTCTCAGGCTCTCTTCTGCTTAAAGTAGCTTTATCCCGAGCGAAT 56
Qy 488 TGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGCAATTTTG 543
Db 55 TGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGCAATTTTG 1
RESULT 17
AX616317/c 2016 bp DNA linear PAT 20-FEB-2003
LOCUS Sequence 1 from Patent WO02094864.
DEFINITION AX616317
ACCESSION AX616317
VERSION AX616317.1 GI:28447361
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Bejanin, S. and Tanaka, H.
TITLE Human cdnas and proteins and uses thereof
JOURNAL Patent: WO 02094864-A 1 28-NOV-2002;
GENSET (FR)
FEATURES
source 1. .2016
/organism="Homo sapiens"
Location/Qualifiers

/mol_type="unassigned DNA"
/db_xref="taxon:9606"
1. .1434
1435. .1839
/note="unnamed protein product"
/codon_start=1
/protein_id="CAD67623.1"
/db_xref="GI:28447362"
/translation="MAACQLLEITLFLRETFSLPRPRTEPLVASTDHTKMPQMEH
AMETMTTFHKFAGDKGLTKEDLRVLMEKEFFPGFLENQKDLPLAVDKIMKLDLQCRDG
KVGFSFSLIAGLTACNDYFVVMKQKGGK"
3'UTR
polyA_signal
polyA_site
2001. .2016
ORIGIN

Query Match 40.5%; Score 485.2; DB 6; Length 2016;
Best Local Similarity 94.7%; Pred. No. 6.7e-93;
Matches 502; Conservative 0; Mismatches 28; Indels 0; Gaps 0;
73 TATTAACTTTCTCTCTGCTGTCATCAATGAGAGTTAGATTTTATTATTTTACATTTGCT 132
Db TTTTCTTTCTCTCTGCTGTCATCAATGAGAGTTAGATTTTATTATTTTACATTTGCT 1953
133 AAGTGTCTGATGCTCATGAATTCCTTCTATGGGGAAGCTGTGGGAGATTCCTTA 192
Db AAGTGTCTGATGCTCATGAATTCCTTCTATGGGGAAGCTGTGGGAGATTCCTTA 1893
193 AGCGACCTTTGGGACACTTATCAGGGAGGAGCACTGCTCATTTCTGCTACTTC 252
Db AGCGACCTTTGGGACACTTATCAGGGAGGAGCACTGCTCATTTCTGCTACTTC 1833
253 TTTCCCTTCTGCTTCATGCTGCTACAAATAGTCAITTCATGCAATGGTGAGGCCCGCA 312
Db TTTCCCTTCTGCTTCATGCTGCTACAAATAGTCAITTCATGCAATGGTGAGGCCCGCA 1773
313 ATTAGGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTCCCTTC 372
Db ATTAGGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCAGTCCCTTC 1713
373 ATTATTTTGTCCAGCAGCGAGGCTTTTGTATTTTCCAAATCCAGGGAATCCCTTT 432
Db ATTATTTTGTCCAGCAGCGAGGCTTTTGTATTTTCCAAATCCAGGGAATCCCTTT 1653
433 TCCATGATCTCTCAGGCTCTCTCTTTGTTAAAGTAGCTTTATCCCGAGCAATTTGTGA 492
Db TCCATGATCTCTCAGGCTCTCTCTTTGTTAAAGTAGCTTTATCCCGAGCAATTTGTGA 1593
493 AATGTAACATCATGTTTCCATGGGTGTTCCATTTGAGATGGCATTTTGGTGTGCTCC 552
Db AATGTAACATCATGTTTCCATGGGTGTTCCATTTGAGATGGCATTTTGGTGTGCTCC 1533
553 GTTCAAGCTTGGCGAGGCGCGGAGCGCTGGCGAGCTGGCGAGCT 602
Db GTTCAAGCTTGGCGAGGCGCGGAGCGCTGGCGAGCTGGCGAGGCT 1483

RESULT 18
LOCUS CQ701466/c 482 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 46392 from Patent WO2070737.
ACCESSION CQ701466
VERSION CQ701466.1 GI:42262233
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 46392 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES
source
Location/Qualifiers
1. .482
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 39.3%; Score 471.6; DB 6; Length 482;
Best Local Similarity 99.2%; Pred. No. 4.5e-90;
Matches 474; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
1 GGAACATAAAAGAACTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAAA 60
Db GAACTTAAAGAAAGAACTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAAA 419
61 AAGCTTATCTGGTATTAACTTTTCTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 120
Db AAGCTTATCTGGTATTAACTTTTCTCTCTGCTGCTCAATGAGAGTTAGATTTTATT 359
121 TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCTCTTATGGGGAAGCTGTGG 180
Db TTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCTCTTATGGGGAAGCTGTGG 299
181 GCAGATTCCTTAAGCAGACCTTTGGGACAACTCTTATCAGGGAGGAGCGAAGCTGCT 240
Db GCAGATTCCTTAAGCAGACCTTTGGGACAACTCTTATCAGGGAGGAGCGAAGCTGCT 239
241 TCTGCCCTACTTCTTCCCTTCTGCTCATGCTGCTACTACAAATAGTCAATGCAATG 300
Db TCTGCCCTACTTCTTCCCTTCTGCTCATGCTGCTACTACAAATAGTCAATGCAATG 179
301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTTACACT 360
Db GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTTACACT 119
361 TCAGGTCTCTTCAATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAATATCCA 420
Db TCAGGTCTCTTCAATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAATATCCA 59
421 GGGAACTCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCC 478
Db GGGAACTCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCTTTATCCC 1

RESULT 19
LOCUS CQ713004/c 472 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 57930 from Patent WO2070737.
ACCESSION CQ713004
VERSION CQ713004.1 GI:42273861
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Liew, C.C., Marshall, W.E. and Zhang, H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 57930 12-SEP-2002;
Chondrogene Inc. (CA)

FEATURES
source
Location/Qualifiers
1. .472
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 38.5%; Score 461.4; DB 6; Length 472;
Best Local Similarity 98.7%; Pred. No. 6.8e-88;
Matches 465; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
73 TATTAACTTTCTCTCTGCTTGTCAAAATGAGATTTAGATTTTATTATTTTACATTTGCT 132
Db TATTAACTTTCTCTCTGCTTGTCAAAATGAGATTTAGATTTTATTATTTTACATTTGCT 132

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Db 472 TATTAACTTTTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATTATTTTACATTTGCT 413
Qy 133 AAGTGCTCCTGATCTGCTCATGAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 192
Db 412 AAGTGCTCCTGATCTGCTCATGAATCCTTCTATGGGGAAGCTGTGGGGCAGATTCCTTA 353
Qy 193 AGCGACCTTTGGGACAACCTTTATCAGGGAGGAGCGAACTGCTCAFTTCTGCTCACTTC 252
Db 352 AGCGACCTTTGGGACAACCTTTATCAGGGAGGAGCGAACTGCTCAFTTCTGCTCACTTC 293
Qy 253 TTTCCCTTCTGCTTCAATGCTACTACAAAATAGTCAATGCAATGCAATGCAATGCAATGCA 312
Db 292 TTTCCCTTCTGCTTCAATGCTACTACAAAATAGTCAATGCAATGCAATGCAATGCAATGCA 233
Qy 313 ATTAGGGAAGAAGCTCTGGAAGCCACCTTCCCATCTCTACACGCTCCAGTCCCTTC 372
Db 232 ATTAGGGAAGAAGCTCTGGAAGCCACCTTCCCATCTCTACACGCTCCAGTCCCTTC 173
Qy 373 ATTATTTTGTCCAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAACCTCCTTT 432
Db 172 GTTATTTTGTCCAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAACCTCCTTT 113
Qy 433 TCCATGAGTACTCTCAGGCTCCTCTTTGTAAGTAGCCTTTATCCCGAGCGAATTTGTGA 492
Db 112 TCCATGAGTACTCTCAGGCTCCTCTTTGTAAGTAGCCTTTATCCCGAGCGAATTTGTGA 53
Qy 493 AATGCTAAACATCATGTTTCCATGGCGTGTTCCATTTGAGATGCGCATTTTG 543
Db 52 AATGTAACATCATGTTTCCATGGCGTGTTCCATTTGAGAGCAATTTTGG 2

RESULT 20
LOCUS CQ704196/c 480 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 49122 from Patent WO02070737.
ACCESSION CQ704196
VERSION CQ704196.1 GI:42264965
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 49122 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1..480
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 37.4%; Score 448; DB 6; Length 480;
Best Local Similarity 95.8%; Pred. No. 4.9e-85;
Matches 460; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

Qy 3 AACTAAAAAGAACTTTATTTATGGGCAAGGGATGCAAAATCAAAAATCAAAA 62
Db 480 ACCTAAAAAGACCTTTATTTATGGGCAAGGGATGCAAAATCAAAAATCAAAA 421
Qy 63 GCTTATCTGTTATTTAACTTTTCTCTGCTGTGCAAAATGAGATTTAGATTTT 122
Db 420 GCTTATCTGTTATTTAACTTTTCTCTGCTGTGCAAAATGAGATTTAGATTT 361
Qy 123 TACATTTGCTAAGTGCTCTGATCTGCTCAATCAATCCTTCTATGGGGAAGCTGTGGGC 182
Db 360 TACATTTGCTAAGTGCTCTGATCTGCTCAATCAATCCTTCTATGGGGAAGCTGTGGGC 301
Qy 183 AGATTCCTTAAGGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCATTT 242
Db 300 AGATTCCTTAAGGACCCCTTTGGGCAACTCTTTATCAGGAGGAGCGAACTGCTCATTT 241
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Qy 243 TGCCTACTTTCTTTCCCTTCTGCTTCTATGTAATACTCAAAAATAGTCAATTCGATCAATGGT 302
Db 240 TGCCTACTTTCTTTCCCTTCTGCTTCTATGTAATACTCAAAAATAGTCAATTCGATCAATGGT 181
Qy 303 GAGGCCCGCAATTTAGGAAAAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTC 362
Db 180 GAGGCCCGCAATTTAGGAAAAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTC 121
Qy 363 CAGGTCCTTCATTTATTTGTCCACGCCAGAGGGTCTTTTGTATTTTCAAAAATCCAGG 422
Db 120 CAGGTCCTTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCAAAAATCCAGG 61
Qy 423 GAACTCCTTTTCCATCAGTACTCTCAGGTCCTCTCTTTTGTAACTAGTCCCTTTATCCCCCAGG 482
Db 60 GAACTCCTTTTCCATCAGTACTCTCAGGTCCTCTCTTTTGTAACTAGTCCCTTTTCCCCCAGG 1

RESULT 21
LOCUS CQ711110/c 474 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 56036 from Patent WO02070737.
ACCESSION CQ711110
VERSION CQ711110.1 GI:42271967
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE Compositions and methods relating to osteoarthritis
JOURNAL Patent: WO 02070737-A 56036 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
source 1..474
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN
Query Match 37.2%; Score 446.4; DB 6; Length 474;
Best Local Similarity 98.9%; Pred. No. 1.1e-84;
Matches 469; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 9 ABAAGAACTTTATTTATTCAGGGCAAGGGATGCAAAACAAAT-ACAAAATCAAAAGCTTA 67
Db 474 AAAAGAACTTTATTTATTCAGGGCAAGGGATGCAAAACAAATCAAAAGCTTA 415
Qy 68 TCTGGTATTATACTTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACAT 127
Db 414 TCTGGTATTATACTTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACAT 355
Qy 128 TTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCGAGATT 187
Db 354 TTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGAAGCTGTGGGCGAGATT 295
Qy 188 CCTTAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCATTTCTGCCT 247
Db 294 CCTTAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCATTTCTGCCT 235
Qy 248 ACTTCTTTTCTCTCTCTCATGTACTACAAAATAGTCAATTCGATGCAATGGTAGGC 307
Db 234 ACTTCTTTTCTCTCTCTCATGTACTACAAAATAGTCAATTCGATGCAATGGTAGGC 175
Qy 308 CGCAATTTAGGGAAGAAAGCTCTGGAAGCCACTTTTGGCATCTCTACACTGCTCAGGT 367
Db 174 CGCAATTTAGGGAAGAAAGCTCTGGAAGCCACTTTTGGCATCTCTACACTGCTCAGGT 115
Qy 368 CTTTCATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAAC 427
Db 114 CTTTCATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAAC 55
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[illegible]

ORGANISM Bos taurus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 Bovinae; Bos.
REFERENCE 1 (bases 1 to 604)
AUTHORS Saris,C.J., Kristensen,T., D'Eustachio,P., Hicks,L.J., Noonan,D.J.,
 Hunter,T. and Tack,B.F.
TITLE cDNA sequence and tissue distribution of the mRNA for bovine and
 murine p11, the S100-related light chain of the protein-tyrosine
 kinase substrate p36 (calpactin I)
JOURNAL J. Biol. Chem. 262 (22), 10663-10671 (1987)
MEDLINE 87280130
PUBMED 3038891
COMMENT Original source text: Bovine intestine epithelial cell, cDNA to
 mRNA.
 Draft entry and printed copy of sequence for [1] kindly provided by
 B.F.Tack, 20-JUL-1987.
 Polyadenylation signals are located at positions 481-486, 525-530
 and 578-583.

FEATURES
 source Location/Qualifiers
 1..604
 /organism="Bos taurus"
 /mol_type="mRNA"
 /db_xref="taxon:9913"
 1..604
 /product="calpactin I lc mRNA"
 /notes="calpactin I light chain"
 /codon_start=1
 /protein_id="AAA30423.1"
 /db_xref="GI:162785"
 /translation="MPSOMEHAMETWMFTPHKFAQDKGYLTKEBRLRVIMEKEFGFPLE
 NOKDPLAVDKIMKDLQCRDQGVQSFSLIAGLTACNDYFVVMHKQKGGK"
 ORIGIN 86 bp upstream of NcoI site.

Query Match	36.2%	Score	434;	DB	4;	Length	604;
Best Local Similarity	88.6%;	Pred.	No. 4.8e-82;				
Matches	505;	Conservative	0;	Mismatches	60;	Indels	5; Gaps 3;

QY 2 GAACAAAAAGAACTTTATTATTGAGGGCAAGGGATGCAAAACATACAAAAATCAA 61
 DB 602 GAACAAAAAGAAATTTGTTTATTGAGCAGAGGATGCAAGCAATATAAAATCAA 543
 QY 62 AGCTTATCTGG---TATTAACTTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTA 118
 DB 542 AGCTTATCTGGCTTTAATTGACITTTCTTCTCTGCTTCTCAAATGAGTTGATTTTA 483
 QY 119 TTTTTCATTTGTGAAGTGTCTGTGATCTGCTCATGAATCTTCTTATGGGGGAAGCTGTG 178
 DB 482 TTTTGTACATTTCTATGGGTCC-CATATGCTCA-GAAATCCTTATACAGGGAGCTGTG 425
 QY 179 GGCAGATTCCTTAAGCGACCTTTGGGCAACTTCTATCAGGTAGGAGCGACTGCTCA 238
 DB 424 GGCAGAGTCTTAAAGTGACCTTTATGAGAAATCTTATCAGGTGGGAGTAATTGCTCA 365
 QY 239 TTTCTGCTACTTCTTTCCCTTCTGCTTTCATGTGACTACAAAATAGCTATTGCATGCA 298
 DB 364 ATGCTGCCTACTTCTTCCCTTCTGCTTTCATGTGACTACAAAATAGCTATTGCATGCGA 305
 QY 299 TGTGAGGCCCGCAATTAGGGAAAGAGCTCTGGAAAGCCACTTTTGCCATCTCTACACT 358
 DB 304 TGTGTAGGCCCAGCGATTAGCGAAAGAGCTCTGGAAAGCCCACTTTTGCCCTCTCGACACT 245
 QY 359 GGTTCAGGTCCTTCATTATTTCGTCCACAGCGAGGGTCTTTTGTATTTTCCAAAAATC 418
 DB 244 GGTTCAGGTCCTTCATTATTTCGTCCACGCGCAGAGGGTCTTTTGTATTTTCCAAAAATC 185
 QY 419 CAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTGTAAAGTACGCTTTATCCC 478
 DB 184 CAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTGTGTAAAGTACCTTTATCAC 125
 QY 479 CAGCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGCGCA 538

Db 124 CTCGAAATTTGTGAAATGTGAACATCATGGTTTCCATGGCTGTCTCCATTTGAGACGGCA 65

QY 539 TTTTGGTGTGGTCCGTTGAAGCCTTGCCG 568

Db 64 TTTTGGTGAAGTCTGTTGAAACCTTGGCG 35

RESULT 24

AX777886/c

LOCUS AX777886 434 bp DNA linear PAT 14-JUL-2003

DEFINITION Sequence 43 from Patent WO03039443.

ACCESSION AX777886

VERSION AX777886.1 GI:32694880

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Haerlach, T., Schoch, C., Kern, W., Kohlmann, A., Schnittger, S., Dugas, M., Eils, R., Brors, B. and Mergenthaler, S.

TITLE Novel genetic markers for leukemias

JOURNAL Patent: WO 03039443-A 43 15-MAY-2003; Deutsches Krebsforschungszentrum (DE); Ludwig-Maximilian-Universitaet Muenchen (DE); Haerlach, Torsten, PD Dr. Dr. (DE); Schoch, Claudia (DE); Kern, Wolfgang (DE)

FEATURES

Location/Qualifiers

source 1..434

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 35.3%; Score 423; DB 6; Length 434;

Best Local Similarity 99.8%; Pred. No. 1e-79;

Matches 434; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 126 ATTTGCTAAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGAGCTGTGGGCGAGA 185

Db 374 TTCTTAAGCGACCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGC 316

QY 186 TTCTTAAGCGACCTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCATTTCTGC 245

Db 374 TTCTTAAGCGACCTTT-GGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTTCTGC 316

QY 246 CTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAATAGTCTATGCAATGTTGAG 305

Db 315 CTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAATAGTCTATGCAATGTTGAG 256

QY 306 GCCCGCAATTAGGAAAAGAGCTCTGGAAGCCACATTTTGGCCATCTTACACTGGTCCAG 365

Db 255 GCCCGCAATTAGGAAAAGAGCTCTGGAAGCCACATTTTGGCCATCTTACACTGGTCCAG 196

QY 366 GTCTTTCATTTATTTGTCCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAA 425

Db 195 GTCTTTCATTTATTTGTCCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAA 136

QY 426 CTCTTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTAACTAGCTTTATCCCGAGGAA 485

Db 135 CTCTTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTAACTAGCTTTATCCCGAGGAA 76

QY 486 TTTGTGAAATGTAAACATCATGGTTTCCATGGGCTGTTCATTTGAGATGGCAATTTTGGT 545

Db 75 TTTGTGAAATGTAAACATCATGGTTTCCATGGGCTGTTCATTTGAGATGGCAATTTTGGT 16

QY 546 GTGGTCCGTTGAAGC 560

Db 15 GTGGTCCGTTGAAGC 1

RESULT 25

HUMP11A/c

LOCUS HUMP11A 480 bp DNA linear PRI 07-JAN-1995

DEFINITION Human p11 protein gene sequence.

ACCESSION M77483

VERSION M77483.1 GI:189420

KEYWORDS p11 protein.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE 1

AUTHORS Harder, T., Kube, E. and Gerke, V.

TITLE Cloning and characterization of the human gene encoding p11: structural similarity to other members of the S-100 gene family

JOURNAL Gene 113 (2), 269-274 (1992)

MEDLINE 92241679

PUBMED 1533380

COMMENT Original source text: Homo sapiens (tissue library: lambda-FixII) DNA.

FEATURES

Location/Qualifiers

source 1..480

/organism="Homo sapiens"

/mol_type="genomic DNA"

/db_xref="taxon:9606"

/cell_type="fibroblast"

/tissue_lib="lambda-FixII"

gene 92..402

/gene="p11"

misc_feature 92..100

/genes="p11"

/note="beta-DRE element"

GC_signal 176..183

/genes="p11"

GC_signal 196..203

/genes="p11"

misc_feature 214..223

/genes="p11"

/note="beta-DRE element"

GC_signal 220..227

/genes="p11"

GC_signal 395..402

/genes="p11"

ORIGIN

Query Match 32.5%; Score 389.2; DB 9; Length 480;

Best Local Similarity 94.6%; Pred. No. 1.7e-72;

Matches 439; Conservative 0; Mismatches 13; Indels 12; Gaps 3;

QY 560 CCTTGGCCGAGGCGCGCGGAGCGCTGGGCGAGCTGGGCGAGC-----TGGACGCGG 610

Db 461 CCTTGGCCGAGGCGCGCGGAGCGCTGGGCGAGCTGGGCGAGCTGGGCGGCGG 402

QY 611 GGCGGAGAGCGGAGCGCGGAGGAGCGCTTGGCGGCGCTCGGCAGGCGCTCTCCCGCAG 730

Db 401 GGCGGAGAGCGGAGCGCGGCGGAGGAGCGCTGGCGGCGCTCGGCAGGCGCTCTCCCGCAG 282

QY 341 AGGAGGCGGCTGGCGGAGCGGAGGAGCGCTGGCGGCGCTCGGCAGGCGCTCTCCCGCAG 282

QY 731 CTGTCTCTCCCTCTCTTCTTCTGCCCCGACCTCCCCCGGCGCGCGGCGCGCCACGC 790

Db 281 CTGTCTCTCCCTCTCTTCTTCTGCCCCGACCTCCCCCGGCGCGCGGCGCGCCACGC 222

QY 791 CTGTCCCTCGCTCCCGGAGCCCGCTCGCAGAGCGCTCGCCCGCCGAGCAGAGCGTTCT 850

Db 221 CTGTCCCTCGCTCCCGGAGCCCGCTCGCAGAGCGCTCGCCCGCCGAGCAGAGCGTTCT 162

QY 851 TGTAAACTTCTCTTTCAGTAGAAACGGTCTCTGCTCTCGAATATTTTCAGGGCATCCCCACCC 910

Db 161 TGTAAACTTCTCTTTCAGTAGAAACGGTCTCTGCTCTCGAATATTT--AGGCGATCCCCACCC 104

QY 911 TGAGCTGCCCTTCTCTCTCGGGTTTGGTTTTAGAAAAGTGTACAAATCAAGAAGACCGGCC 970

Db 103 TGAGCTGCCCTTCTCTCTCGGGTTTGGTTTTAGAAAAGTGTACAAATCAAGAAGACCGGCC 44

REFERENCE
AUTHORS Ihiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H., Takahashi,T., Imai,K., Hiraesawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Teujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
TITLE Characterization of gene expression profiles in early bovine pregnancy using a custom cDNA microarray
JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)
MEDLINE 22544902
PUBMED 12658628
REFERENCE 2 (bases 1 to 534)
AUTHORS Teujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K., Hiraesawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y., Todoroki,J. and Hashizume,K.
TITLE Direct Submission
JOURNAL Submitted (25-DEC-2002) Gozoh Teujimoto, National Research Institute for Child Health and Development, Department of Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan (E-mail: gtsujimoto@nch.go.jp, Tel:81-3-3149-2476, Fax:81-3-3149-1252)
COMMENT This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuhisa@affrc.go.jp
This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and Technology.
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Qy 302 TGAGGCCCGCAATTAGGGAAAAGAAAGCTCTGGAAGGCCCACTTTTGGCAATCTCTACACTGGT 361

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AUTHORS Ihiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H., Takahashi,T., Imai,K., Hiraesawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Teujimoto,G., Izaike,Y., Todoroki,J. and Hashizume,K.
TITLE Characterization of gene expression profiles in early bovine pregnancy using a custom cDNA microarray
JOURNAL Mol. Reprod. Dev. 65 (1), 9-18 (2003)
MEDLINE 22544902
PUBMED 12658628
REFERENCE 2 (bases 1 to 534)
AUTHORS Teujimoto,G., Ishiwata,H., Katsuma,S., Kizaki,K., Patel,O.V., Nakano,H., Konno,T., Ushizawa,K., Takahashi,T., Imai,K., Hiraesawa,A., Shiojima,S., Ikawa,H., Suzuki,Y., Izaike,Y., Todoroki,J. and Hashizume,K.
TITLE Direct Submission
JOURNAL Submitted (25-DEC-2002) Gozoh Teujimoto, National Research Institute for Child Health and Development, Department of Molecular, Cell Pharmacology; 3-35-31 Taishido, Setagaya, Tokyo 154-8567, Japan (E-mail: gtsujimoto@nch.go.jp, Tel:81-3-3149-2476, Fax:81-3-3149-1252)
COMMENT This work was performed to collaborate with Developmental Biology Department, National Institute of Agrobiological Sciences. Address: 2 Ikenodai, Tsukuba, Ibaraki, 305-8602 Japan. Phone & Fax: 81-29-838-8633 e-mail: kazuhisa@affrc.go.jp
This work was funded by Organized Research Combination System (ORCS) project of Ministry of Education, Culture, Sports, Science and Technology.
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REFERENCE
AUTHORS      Liew,C.C., Marshall,W.E. and Zhang,H.
TITLE        Compositions and methods relating to osteoarthritis
JOURNAL      Patent: WO 02070737-A 51172 12-SEP-2002; Chondrogene Inc. (CA)

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Db   184 GCAGATTCCTTAGCGCACCTTTGGGACACTCTTATCAGGGAGGAGCGAACTGCTCATTT 125

Qy   241 TCTGCCCTACTCTTCCTCCCTTCCTCTCATGTGTACTACAAAATAGTCATTGCGATGCAATG 300
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         4 TC CA 1

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LOCUS      AX306168             600 bp            DNA           linear      PAT 11-DEC-2001
DEFINITION Sequence 919 from Patent WO0188188.
ACCESSION AX306168
VERSION    AX306168.1 GI:17645451
KEYWORDS
SOURCE     Mus musculus (house mouse)
ORGANISM   Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
1 Ishikawa,K., Asai,S., Takahashi,Y., Nagata,T. and Ishii,Y.
METHOD     Method for examining ischemic conditions
PATENT     Patent: WO 0188188-A 919 22-NOV-2001; School Juridical Person Nihon University (JP)

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QY 369 CTTCAATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAATCCAGGGAATC 428
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QY 429 CTTTTCATGAGTACTCTCAGGCTCTCTTGTGTTTAACTAGTCCCTTATCCCGAGCAATTT 488
Db 130958 CTTTCCATGAGTACTTTCAGGCTCTCTTCAATTAAGTACCTTATCCCGGCAATCT 131017
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DEFINITION Sequence 56710 from Patent WO02070737.
ACCESSION CO711784
VERSION CO711784.1 GI:42272641
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
Liew,C.C., Marshall,W.E. and Zhang,H.
Compositions and methods relating to osteoarthritis
Patent: WO 02070737-A 56710 12-SEP-2002;
Chondrogene Inc. (CA)
FEATURES
Location/Qualifiers
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Matches 458; Conservative 0; Mismatches 107; Indels 24; Gaps 4;

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Best Local Similarity 100.0%; Pred. No. 6.8e-60;
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LOCUS BD251901 600 bp DNA linear PAT 17-JUL-2003
DEFINITION Potassium channel interactors and uses therefor.
ACCESSION BD251901
VERSION BD251901.1 GI:33061671
KEYWORDS JP 2002530104-A/34.
SOURCE Rattus sp.
ORGANISM Rattus
REFERENCE
1 (bases 1 to 600)
Rhodes,K., Betty,W., Ling,H.P. and An,W.
Potassium channel interactors and uses therefor
Patent: JP 2002530104-A 34 17-SEP-2002;
MILLENNIUM PHARMACEUTICALS INC,AMERICAN HOME PRODUCTS CORP
OS Rattus sp. (rat)
PN JP 2002530104-A/34
PD 17-SEP-2002
PF 19-NOV-1999 JP 2000583959
PR 20-NOV-1998 US 60/109333,25-NOV-1998 US 60/110033 PR
30-NOV-1998 US 60/110277,23-APR-1999 US 09/298731 PR
09-JUL-1999 US 09/350614,09-JUL-1999 US 09/350874 PR
21-SEP-1999 US 09/399913,21-SEP-1999 US 09/400492 PI
KENNETH RHODES,MARIA BETTY,HUAI PING LING,WENQIAN AN PC
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PC A61P43/00,C07K14/47,C07K16/18,C12N5/10,C12P21/02,C12Q1/68, PC
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VERSION	AR473726.1	GI:42712140			
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SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 600)				
AUTHORS	Rhodes, K., Betty, M., Ling, H.-P. and An, W.				
TITLE	Potassium channel interactors and uses therefor				
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AUTHORS	Rhodes, K., Betty, M., Ling, H.-P. and An, W.				
TITLE	Nucleic acid molecules encoding potassium channel interactors and uses therefor				
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

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Gapop 10.0 , Gapext 1.0

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Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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- 3: Geneseqn2000s.*
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- 12: Geneseqn2004as.*
- 13: Geneseqn2004bs.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1199	100.0	1199	12	ADP67435 Human p11
c 2	1199	100.0	1199	12	ADP67436 Human p11
c 3	1199	100.0	1199	12	ADQ84359 Human tum
c 4	1199	100.0	1199	13	ACN37451 Tumour-as
c 5	703.4	58.7	1124	8	ABX63001 Human CDN
c 6	634	52.9	1893	3	AACT78192 Human can
c 7	634	52.9	1893	3	AACT78192 Human can
c 8	601	50.1	649	3	AAA46679 Human col
c 9	601	50.1	649	3	AAA46679 Human col
c 10	601	50.1	649	10	ADN18599 Human dis
c 11	601	50.1	649	10	ADN18599 Human dis
c 12	601	50.1	649	10	ADN18599 Human dis
c 13	601	50.1	649	13	ADN18599 Human dis
c 14	601	50.1	649	13	ADN18599 Human dis
c 15	601	50.1	649	13	ADN18599 Human dis
c 16	595.8	49.7	663	6	ABQ55234 Human ova
c 17	557	46.5	579	3	AAA46667 Human ova
c 18	537	44.8	571	6	ABK45339 Human ova
c 19	523	43.6	582	3	AACT10823 Human sec
c 20	516.8	43.1	530	10	ADK11670 Breast ca

c 21	485.2	40.5	2016	8	ACC51060	Acc51060 Human S-1
c 22	429.4	35.8	477	9	ACH34296	Ach34296 Human end
c 23	423	35.3	434	10	ADF79487	Adf79487 Leukaemia
c 24	422	35.2	466	9	ACH25344	Ach25344 Human adu
c 25	411	34.3	441	4	AAF75092	Aaf75092 Human col
c 26	396.2	33.0	632	4	AAH53326	Aah53326 Human col
c 27	347.4	29.0	350	10	ADK11672	Adk11672 Breast ca
c 28	343.6	28.7	600	6	ABI99809	Abi99809 Mouse isc
c 29	339.4	28.3	341	10	ADK11671	Adk11671 Breast ca
c 30	329.8	27.5	600	3	AAA46561	Aaa46561 cDNA sequ
c 31	329.8	27.5	600	6	ABK72684	Abk72684 DNA encod
c 32	329.2	27.5	573	6	ABK63467	Abk63467 Rat seque
c 33	329.2	27.5	573	10	ADB58585	Adb58585 Toxicity-
c 34	329.2	27.5	573	10	ADB53216	Adb53216 Primary r
c 35	329.2	27.5	573	10	ABT42181	Abt42181 Toxicity
c 36	329.2	27.5	573	10	ABX13102	Abx13102 Rat cDNA
c 37	329.2	27.5	573	12	ADP72563	Adp72563 Renal tox
c 38	317	26.4	318	4	AA557410	Aas57410 cDNA #86
c 39	294	24.5	294	3	AAAC81810	Aac81810 Human S10
c 40	291	24.3	291	9	ADA08452	Ada08452 Mammalian
c 41	291	24.3	291	9	ADA08453	Ada08453 Mammalian
c 42	291	24.3	291	12	ADP67424	Adp67424 Human p11
c 43	291	24.3	291	12	ADP67425	Adp67425 Human p11
c 44	273.8	22.8	464	4	AAI10124	Aai10124 Probe #57
c 45	273.8	22.8	464	4	ABA51754	Aba51754 Human foe

ALIGNMENTS

RESULT 1

ADP67435

ID ADP67435 standard; cDNA; 1199 BP.

XX AC ADP67435;

XX DT 23-SEP-2004 (first entry)

XX DE Human p11 antisense polynucleotide SEQ ID NO:16.

XX KW p11; p11 activity modulator; plasminogen activation; cytostatic;

XX KW antisense therapy; cancer; tumour; tumour growth inhibition; human;

XX KW antisense; gene; ds.

XX OS Homo sapiens.

XX PN WO2004054517-A2.

XX PD 01-JUL-2004.

XX PF 12-DEC-2003; 2003WO-US040029.

XX PR 13-DEC-2002; 2002US-0433140P.

XX PA (MEDI-) MEDIONICS LLC.

XX PI (WAIS/) WAISMAN D.

XX PI Waisman D;

XX DR WPI; 2004-487995/46.

XX PT Composition useful for inhibiting growth of tumor in patient, modulates

XX PT activity of p11 protein and effects change in level of plasminogen

XX PT activation by a cell.

XX PS Claim 5; SEQ ID NO 16; 140pp; English.

XX CC The present invention describes a composition (I) which modulates the

XX CC activity of a p11 protein and effects a change in the level of

XX CC plasminogen activation by a cell. Also described: (1) making (M1) a

XX CC clonal cell line, which involves isolating a cell, then characterizing

XX CC the activity of a protein produced by the cell or clonal progeny of the

XX CC cell, where the protein is involved in plasminogen activation; and (2) a

clonal cell line (II) useful in the identification of composition that modulate p11 activity, where the clonal cell line is obtained by (M1). (I) has cytostatic activity, and can be used in antisense therapy. (I) is useful for modulating the activity of p11 which involves administering (I) to a cell. The cell can be a human cancer cell, chosen from a Hri080 fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal adenocarcinoma cell. (I) is also useful for reducing the development of cancer in a patient e.g., mouse which involves administering (I) to a cancer cell in the patient. (I) is useful for inhibiting the growth of tumours or inhibiting tumour cell invasion in a patient, which involves administering (I) to a cancer cell in the patient. (II) is useful for identifying a composition that modulates p11 activity which involves administering the composition to (II) obtained by (M1), determining the change in p11 activity of a cell of the clonal cell line relative to a cell of a clonal cell line that had not received the composition, and identifying the composition that produces a change in p11 activity. The change in p11 activity is a change in the level of plasminogen activation activity. The present sequence represents a p11 antisense polynucleotide, which is used in the exemplification of the present invention.

Sequence 1199 BP; 235 A; 338 C; 337 G; 289 T; 0 U; 0 Other

Query Match	100.0%;	Score 1199;	DB 12;	Length 1199;
Best Local Similarity	100.0%;	Pred. No. 3.3e-293;		
Matches 1199;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GGAACTTAAAGAAAGACTTTATTATTGAGGCGAAGGGATGCCAAACATACAAAATCAA	60	
DB	1	GGAACTTAAAGAAAGACTTTATTATTGAGGCGAAGGGATGCCAAACATACAAAATCAA	60	
QY	61	AAGCTTATCTGGTATTAAACTTTTCTTCTCTGCTGCTCAAATGAGAGTTAGATTTTATT	120	
DB	61	AAGCTTATCTGGTATTAAACTTTTCTTCTCTGCTGCTCAAATGAGAGTTAGATTTTATT	120	
QY	121	TTTACATTTGCTAAGTGTCTTGATCTGCTCATGAAATCTTCTATGSGGGAGACTGTGG	180	
DB	121	TTTACATTTGCTAAGTGTCTTGATCTGCTCATGAAATCTTCTATGSGGGAGACTGTGG	180	
QY	181	CGAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT	240	
DB	181	CGAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAT	240	
QY	241	TCTGCTACTTCTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCATTTCGATGCAATG	300	
DB	241	TCTGCTACTTCTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCATTTCGATGCAATG	300	
QY	301	GTGAGGCGCGCAATTAGGGAAAGAGCTCTGGAGGCCCACTTTGGCACTCTACACTGG	360	
DB	301	GTGAGGCGCGCAATTAGGGAAAGAGCTCTGGAGGCCCACTTTGGCACTCTACACTGG	360	
QY	361	TCCAGGTCTTCAATTATTTTGTTCACAGCCAGAGGGTCTTTTGTATTTCCAAAATCCA	420	
DB	361	TCCAGGTCTTCAATTATTTTGTTCACAGCCAGAGGGTCTTTTGTATTTCCAAAATCCA	420	
QY	421	GGAACTCTCTTTTCCATCAGTACTCTCAGTGCCTCTCTTTGTTAAGTAGCCCTTTATCCCCA	480	
DB	421	GGAACTCTCTTTTCCATCAGTACTCTCAGTGCCTCTCTTTGTTAAGTAGCCCTTTATCCCCA	480	
QY	481	CGCAATTTGTGAAATGTAAACATCATGTGTTTCCATGCGTGTGTCCATTGAGATGGCAT	540	
DB	481	CGCAATTTGTGAAATGTAAACATCATGTGTTTCCATGCGTGTGTCCATTGAGATGGCAT	540	
QY	541	TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGGCGCGGGAGCGCTGGGCGAGCTGGGCGAG	600	
DB	541	TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGGCGCGGGAGCGCTGGGCGAGCTGGGCGAG	600	
QY	601	CTTGGACGCGGGGCGAGAGGCGAGCGCGCGGCTGTGCGCTCTTCTCTAGTACGTCGCGC	660	
DB	601	CTTGGACGCGGGGCGAGAGGCGAGCGCGCGGCTGTGCGCTCTTCTCTAGTACGTCGCGC	660	
QY	661	GGTGGGTAGAGGAGCGCGCGGAGCGGAGCGAGCGCTGGGCGGCGCTCGCGAGGGCG	720	
DB	661	GGTGGGTAGAGGAGCGCGCGGAGCGGAGCGAGCGCTGGGCGGCGCTCGCGAGGGCG	720	

Qy	721	CTCCCCAGCCCTGTCTCTCTCCCCCTCTTCTCTGCCCCCGACTCCCCGACCCCGGGGCGG	780
Db	721	CTCCCCAGCCCTGTCTCTCTCCCCCTCTTCTCTGCCCCCGACTCCCCGACCCCGGGGCGG	780
Qy	781	CGGCCACGCCCTGCCTCGCTCCCGACCCGCTCGCAGAGCGCTCGCCGCCCCAGAC	840
Db	781	CGGCCACGCCCTGCCTCGCTCCCGACCCGCTCGCAGAGCGCTCGCCGCCCCAGAC	840
Qy	841	AGAGCGTTCTTGTAACCTCTCTCAGTAGAAACGGTCTGTCTCGAATATTTTCAGGGC	900
Db	841	AGAGCGTTCTTGTAACCTCTCTCAGTAGAAACGGTCTGTCTCGAATATTTTCAGGGC	900
Qy	901	ATCCCCACCTGAGCCTGCCCTTCTCTCGGTTTGGTTTTAGAAAGTGACAAATCAA	960
Db	901	ATCCCCACCTGAGCCTGCCCTTCTCTCGGTTTGGTTTTAGAAAGTGACAAATCAA	960
Qy	961	GAACCCGGCCGCTCTCTCGGGTGGGGACGCTGGCGCAGAACACAGAGTAACCGGCTCTGC	1020
Db	961	GAACCCGGCCGCTCTCTCGGGTGGGGACGCTGGCGCAGAACACAGAGTAACCGGCTCTGC	1020
Qy	1021	GGCCACCTACGGGTCTAGGAATTACTTGTCTGATGACCTTGACAGGAGTGGCAGTGGAG	1080
Db	1021	GGCCACCTACGGGTCTAGGAATTACTTGTCTGATGACCTTGACAGGAGTGGCAGTGGAG	1080
Qy	1081	TCCTATCGACTCAGAGGCCACTATCAGATTAGCCCTAGGAGTCCCGTCTGGGGGTCTCGG	1140
Db	1081	TCCTATCGACTCAGAGGCCACTATCAGATTAGCCCTAGGAGTCCCGTCTGGGGGTCTCGG	1140
Qy	1141	CGGCGTGGCCAGTGGAGGGCGGCACTTCTCCCGAAGCGCGGCTTCCCGCCCCACCGG	1199
Db	1141	CGGCGTGGCCAGTGGAGGGCGGCACTTCTCCCGAAGCGCGGCTTCCCGCCCCACCGG	1199

RESULT 2	
ADP67436/c	
ID	ADP67436 standard; cDNA; 1199 BP.
XX	
XX	
AC	ADP67436;
XX	
DT	23-SEP-2004 (first entry)
XX	
DE	Human p11 sense polynucleotide SEQ ID NO:17.
XX	
KW	p11; p11 activity modulator; plasminogen activation; cytostatic;
KW	antisense therapy; cancer; tumour; tumour growth inhibition; human; gene;
KW	ds.
XX	
XX	
OS	Homo sapiens.
XX	
PN	WO2004054517-A2.
XX	
PD	01-JUL-2004.
XX	
PF	12-DEC-2003; 2003WO-US040029.
XX	
PR	13-DEC-2002; 2002US-0433140P.
XX	
PA	(MEDI-) MEDIMICS LLC.
PA	(WAIS/) WAISMAN D.
XX	
PI	Waisman D;
XX	
DR	WPI; 2004-487995/46.
XX	
PT	Composition useful for inhibiting growth of tumor in patient, modulates
PT	activity of p11 protein and effects change in level of plasminogen
PT	activation by a cell.
XX	
PS	Claim 16; SEQ ID NO 17; 140pp; English.
XX	
CC	The present invention describes a composition (I) which modulates the
CC	activity of a p11 protein and effects a change in the level of

CC plasminogen activation by a cell. Also described: (1) making (M1) a
CC clonal cell line, which involves isolating a cell, then characterising
CC the activity of a protein produced by the cell or clonal progeny of the
CC cell, where the protein is involved in plasminogen activation; and (2) a
CC clonal cell line (II) useful in the identification of composition that
CC modulate p11 activity, where the clonal cell line is obtained by (M1);
CC (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC useful for modulating the activity of p11 which involves administering
CC (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC fibrosarcoma cell, a LNCaP prostate cancer cell, and a CCL-22 colorectal
CC adenocarcinoma cell. (I) is also useful for reducing the development of
CC cancer in a patient e.g., mouse which involves administering (I) to a
CC cancer cell in the patient. (I) is useful for inhibiting the growth of
CC tumours or inhibiting tumour cell invasion in a patient, which involves
CC administering (I) to a cancer cell in the patient. (II) is useful for
CC identifying a composition that modulates p11 activity which involves
CC administering the composition to (II) obtained by (M1), determining the
CC change in p11 activity of a cell of the clonal cell line relative to a
CC cell of a clonal cell line that had not received the composition, and
CC identifying the composition that produces a change in p11 activity. The
CC change in p11 activity is a change in the level of plasminogen activation
CC activity. The present sequence represents a p11 sense polynucleotide,
CC which is used in the exemplification of the present invention.
XX
SQ Sequence 1199 BP; 289 A; 337 C; 338 G; 235 T; 0 U; 0 Other;

Query Match 100.0%; Score 1199; DB 12; Length 1199;
Best Local Similarity 100.0%; Pred. No. 3.3e-293;
Matches 1199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAACCTAAAAGAACCTTTATTTATGAGGCAAGGGATGCAAAACATCAAAAATCAA 60
Db 1199 GGAACCTAAAAGAACCTTTATTTATGAGGCAAGGGATGCAAAACATCAAAAATCAA 1140

Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGTGCAAAATCAGAGTTAGATTTTATT 120
Db 1139 AAGCTTATCTGGTATTTAACTTTTCTCTGCTGTGCAAAATCAGAGTTAGATTTTATT 1080

Qy 121 TTTACATTTGCTAAGTGTCTGTATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180
Db 1079 TTTACATTTGCTAAGTGTCTGTATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 1020

Qy 181 GCAGATTCCTTAAGGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCAATT 240
Db 1019 GCAGATTCCTTAAGGACCCCTTTGGGACAACTTTATCAGGAGGAGCGAACTGCTCAATT 960

Qy 241 TCTGCTACTTCTTTTCCCTTCTGCTTCTATGCTGTACTACAAATAGTATTCATGCAATG 300
Db 959 TCTGCTACTTCTTTTCCCTTCTGCTTCTATGCTGTACTACAAATAGTATTCATGCAATG 900

Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGGCCCACTTTGGCCATCTCTACACTGG 360
Db 899 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGGCCCACTTTGGCCATCTCTACACTGG 840

Qy 361 TCCAGGTCTCTTATTTTGTTCACAGCCAGAGGGTCTTTTGAATTTCCAAAATCCCA 420
Db 839 TCCAGGTCTCTTATTTTGTTCACAGCCAGAGGGGTCTTTTGAATTTCCAAAATCCCA 780

Qy 421 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTTGTGTTAAGTAGCCCTTTATCCCCA 480
Db 779 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTTGTGTTAAGTAGCCCTTTATCCCCA 720

Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTTCCTTTGAGATGGCAATT 540
Db 719 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTGTTCCTTTGAGATGGCAATT 660

Qy 541 TTGGTGTGGTCCGTTGAAGCCCTTGGCCAGCGCGCGGACGCTGGGCGAGCTGGGCGAG 600
Db 659 TTGGTGTGGTCCGTTGAAGCCCTTGGCCAGCGCGCGGACGCTGGGCGAGCTGGGCGAG 600

Qy 601 CTGACCGCGGGCGAGGCGGCGGCGGCTGTGCGCTTCTCTAGTACGTGCGGC 660
Db 599 CTGACCGCGGGCGAGGCGGCGGCGGCTGTGCGCTTCTCTAGTACGTGCGGC 540

Qy 661 GGGTGGGTAGAGGAGGCGCGCGGGAGCGGAGGAGCCTTGGCGGGGCGCTCGGAGGGCG 720
Db 539 GGGTGGGTAGAGGAGGCGCGCGGGAGCGGAGGAGCCTTGGCGGGGCGCTCGGAGGGCG 480

Qy 721 CTGCCCCAGCCCTGTCTCCCTTCTCCCTTCTTCTGTCGCCCGGACTCCCGGAGCCCGGGGCG 780
Db 479 CTGCCCCAGCCCTGTCTCCCTTCTCCCTTCTTCTGTCGCCCGGACTCCCGGAGCCCGGGGCG 420

Qy 781 CGGCCCCAGCCCTGCTCCCTTCTCCGACCCGCTCGCAGAGGCTCGCGCCGCCAGAC 840
Db 419 CGGCCCCAGCCCTGCTCCCTTCTCCGACCCGCTCGCAGAGGCTCGCGCCGCCAGAC 360

Qy 841 AGAGCGTTCTTTGTAACCTTCTTTCAGTAGAAGACGGTCTCTCGAATATTTTCAGGGC 900
Db 359 AGAGCGTTCTTTGTAACCTTCTTTCAGTAGAAGACGGTCTCTCGAATATTTTCAGGGC 300

Qy 901 ATCCCCACCTTGAGCCCTGCCCCCTTCTCTCGGGTTTGGTTTTAGAAAGTGTACAAATCAA 960
Db 299 ATCCCCACCTTGAGCCCTGCCCCCTTCTCTCGGGTTTGGTTTTAGAAAGTGTACAAATCAA 240

Qy 961 GAAACCGGCGCTCTGCGGGTGGGCAACGCTGGCGCAAGACAGAGGTAAACCGGCTCTGC 1020
Db 239 GAAACCGGCGCTCTGCGGGTGGGCAACGCTGGCGCAAGACAGAGGTAAACCGGCTCTGC 180

Qy 1021 GGCCACCTACGGGTCTAGGAATTTACTTGTGGATGACCTTGCAGGGAGTGGCACGTGGAG 1080
Db 179 GGCCACCTACGGGTCTAGGAATTTACTTGTGGATGACCTTGCAGGGAGTGGCACGTGGAG 120

Qy 1081 TCCTATGACCTCAGAGGCACTATCAGATTAGCCCTTAGGAGTCCGCTCTGCGGGTCTCGG 1140
Db 119 TCCTATGACCTCAGAGGCACTATCAGATTAGCCCTTAGGAGTCCGCTCTGCGGGTCTCGG 60

Qy 1141 CGGCTGCGGCACTGGAAGGGCGGCACTCCCGCAGAAAGCGGCTTCCCGCCCGCCACCG 1199
Db 59 CGGCTGCGGCACTGGAAGGGCGGCACTCCCGCAGAAAGCGGCTTCCCGCCCGCCACCG 1

RESULT 3
ADQ84359/c
ID ADQ84359 standard; cDNA; 1199 BP.
XX ADQ84359;
AC ADQ84359;
XX 07-OCT-2004 (first entry)
DT Human tumour-associated antigenic target (TAT) cDNA sequence #1173.
XX human; tumour-associated antigenic target; TAT; cytostatic; gene therapy;
XX cancer; cell proliferative disorder; gene; ss.
OS Homo sapiens.
XX WO2004060270-A2.
PN 22-JUL-2004.
PD 15-OCT-2003; 2003WO-US029126.
PP 18-OCT-2002; 2002US-0418988P.
PR (GETH) GENENTECH INC.
PA (WUTD/) WU T D.
PA (ZHOU/) ZHOU Y.
XX Wu TD, Zhou Y;
XX WPI; 2004-534300/51.
DR New nucleic acid molecule and encoded polypeptide, for diagnosing,
PT preventing or treating cell proliferative disorders such as cancer.
XX Claim 1; SEQ ID NO 1173; 5504pp; English.
PS

XX WO2004030615-A2.
 XX 15-APR-2004.
 XX 29-SEP-2003; 2003WO-US028547.
 XX 02-OCT-2002; 2002US-0414971P.
 XX (GETH) GENENTECH INC.
 XX Wu TD, Zhang Z, Zhou Y;
 XX WPI; 2004-347921/32.
 DR P-PSDB; ABM80135.
 XX
 PT New tumor-associated antigenic target polypeptides and nucleic acids,
 PT useful in preparing a medicament for treating or detecting a
 PT proliferative disorder, e.g. breast, lung, colorectal, ovarian or
 PT prostate cancer or tumor.
 XX
 PS Claim 1; SEQ ID NO 342; 7273pp; English.
 XX
 CC The invention relates to human tumour-associated antigenic target (TAT)
 CC polypeptides, and their related nucleic acids. The TAT polypeptides are
 CC overexpressed in cancer tissues compared to normal tissues, and may thus
 CC serve as effective targets for the diagnosis and treatment of cancer in
 CC mammals. The invention also relates to nucleic acid and polypeptide
 CC sequences at least 80% identical to the TAT nucleic acids and
 CC polypeptides; expression vectors and host cells comprising a TAT nucleic
 CC acid; an antibody specific for a TAT polypeptide; a peptide or organic
 CC molecule which binds to a TAT polypeptide; fusion proteins comprising a
 CC TAT polypeptide; and methods and compositions for the treatment or
 CC diagnosis of cancer in mammals. TAT polypeptides, nucleic acids,
 CC antibodies, antagonists, binding molecules and compositions are useful
 CC for diagnosing or treating a cell proliferative disorder associated with
 CC increased TAT expression, particularly cancers such as breast cancer,
 CC colorectal cancer, lung cancer, ovarian cancer, liver cancer, bladder
 CC cancer, pancreatic cancer, cervical cancer, cancers of the central
 CC nervous system, melanoma and leukaemia. TAT nucleic acids may further be
 CC used as hybridisation probes, in chromosome and gene mapping, in
 CC chromosome identification and in gene therapy. The present sequence
 CC represents a TAT nucleic acid of the invention
 XX
 SQ Sequence 1199 BP; 289 A; 337 C; 338 G; 235 T; 0 U; 0 Other;
 Query Match 100.0%; Score 1199; DB 13; Length 1199;
 Best Local Similarity 100.0%; Pred. No. 3.3e-293;
 Matches 1199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAACTAAAAAGAACTTTTATTATTGAGGCAAGGGATGCAAAACAATACAAAATCAA 60
 Db 1199 GGAACTAAAAAGAACTTTTATTATTGAGGCAAGGGATGCAAAACAATACAAAATCAA 1140
 Qy 61 AAGCTTATCTGGTATTTAACTTTTCTTCTGCTGCTCAAAATGAGATTTAGTTTATT 120
 Db 1139 AAGCTTATCTGGTATTTAACTTTTCTTCTGCTGCTCAAAATGAGATTTAGTTTATT 1080
 Qy 121 TTTTACATTTGCTAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGAAGCTGTGGG 180
 Db 1079 TTTTACATTTGCTAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGAAGCTGTGGG 1020
 Qy 181 GCAGATTCCTTAAAGCACCTTTTGGGACAACTTTATCAGGAGGAGCGAAGTCTCATTT 240
 Db 1019 GCAGATTCCTTAAAGCACCTTTTGGGACAACTTTATCAGGAGGAGCGAAGTCTCATTT 960
 Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCTGATGTAATCAAAATAGTCAATGCAATG 300
 Db 959 TCTGCCTACTTCTTCCCTTCTGCTTCTGATGTAATCAAAATAGTCAATGCAATG 900
 Qy 301 GTGAGGCCGCAATTAGGAAAAGAACTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
 Db 899 GTGAGGCCGCAATTAGGAAAAGAACTCTGGAAGCCCACTTTGCCATCTCTACACTGG 840

Qy 361 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAAATCCA 420
 Db 839 TCCAGGTCCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTGATTTTCCAAAAATCCA 780
 Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTTCTTAAAGTAGTCTTTATCCCA 480
 Db 779 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTTCTTAAAGTAGTCTTTATCCCA 720
 Qy 481 GCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTAGATGGCAATT 540
 Db 719 GCGAATTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTAGATGGCAATT 660
 Qy 541 TTGGTGTGGTCCGTGTGAAGCCTTTGGCCGAGCGCGCGGACGCTGGCGAGCTGGGCGAG 600
 Db 659 TTGGTGTGGTCCGTGTGAAGCCTTTGGCCGAGCGCGCGGACGCTGGCGAGCTGGGCGAG 600
 Qy 601 CTGGACCGGGGGGGAGAGCGGCGGCGGCTGTGCGCTTCTTAGTAGCTGCGGCG 660
 Db 599 CTGGACCGGGGGGGAGAGCGGCGGCGGCTGTGCGCTTCTTAGTAGCTGCGGCG 540
 Qy 661 GGGTGGGTAGAGGAGCGCGCGGAGCGGAGGAGGCTGGCGGGGCTCGGCGAGGCG 720
 Db 539 GGGTGGGTAGAGGAGCGCGCGGAGCGGAGGAGGCTGGCGGGGCTCGGCGAGGCG 480
 Qy 721 CTCCCCAGCCCTGTCTCTCTCCCCCTTCTTCTGCCCCGACTCCCGGACCCCGGGGCG 780
 Db 479 CTCCCCAGCCCTGTCTCTCTCCCCCTTCTTCTGCCCCGACTCCCGGACCCCGGGGCG 420
 Qy 781 CGGCCCAAGCCCTGCTCTCGGACCGGCTCGCAGAGGCTCGCGCGGCGCCAGAC 840
 Db 419 CGGCCCAAGCCCTGCTCTCGGACCGGCTCGCAGAGGCTCGCGCGGCGCCAGAC 360
 Qy 841 AGAGCGTCTTTGTAACCTTCTTCTAGTAGAAGCGTCTGCTCTCGAATATTTACAGGC 900
 Db 359 AGAGCGTCTTTGTAACCTTCTTCTAGTAGAAGCGTCTGCTCTCGAATATTTACAGGC 300
 Qy 901 ATCCCCACCTTGAGCTGCCCCCTTCTCTCGGGTTTGGTTTAAAGAGTGTAACAATCAA 960
 Db 299 ATCCCCACCTTGAGCTGCCCCCTTCTCTCGGGTTTGGTTTAAAGAGTGTAACAATCAA 240
 Qy 961 GAACCCGGCGCTCTCGGGTGGGACGCTGGCGGAGAGGAGGTAACCGGCTCTGC 1020
 Db 239 GAACCCGGCGCTCTCGGGTGGGACGCTGGCGGAGAGGAGGTAACCGGCTCTGC 180
 Qy 1021 GGCACCTACGGGTCTAGGAATTTACTTGTGATGACCTTGAGGAGTGCGACGTGGAG 1080
 Db 179 GGCACCTACGGGTCTAGGAATTTACTTGTGATGACCTTGAGGAGTGCGACGTGGAG 120
 Qy 1081 TCTATCGACCTCAGAGGCACTATCAGATTAGCCCTAGGAGGTCCGCTCTGGGGTCTCGG 1140
 Db 119 TCTATCGACCTCAGAGGCACTATCAGATTAGCCCTAGGAGGTCCGCTCTGGGGTCTCGG 60
 Qy 1141 CGGCTCTGGCAGTGAGGGGGCGGACCTCCCGAGAGCCGGGCTTCCCGCCCGCCACCG 1199
 Db 59 CGGCTCTGGCAGTGAGGGGGCGGACCTCCCGAGAGCCGGGCTTCCCGCCCGCCACCG 1
 RESULT 5
 ABX63001/c
 ID ABX63001 standard; cDNA; 1124 BP.
 XX
 AC ABX63001;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Human cDNA #1 differentially expressed in activated vascular tissue.
 XX
 KW Human; gene; ss; vascular tissue; cytostatic; atherosclerosis; cardiant;
 KW hypotensive; antidiabetic; gynaecological; vasotropic; cerebroprotective;
 KW gene therapy; vascular disease; cancer; coronary; artery disease;
 KW hypertension; diabetes; pre-eclampsia; restenosis;
 KW ischaemia-reperfusion injury; stroke.

1596	TCTGCCTACTCTCTTCCCTCTGCTTCATGTGTACTACAAAATAGTGCATTGCGATGCAATG	1537
301	GTGAGGCCCGCAATTAGGGAAAAAGAGCTCTGGAAGCCCACTTTGGCCATCTCTACACTGG	360
1536	GTGAGGCCCGCAATTAGGGAAAAAGAGCTCTGGAAGCCCACTTTGGCCATCTCTACACTGG	1477
361	TCGAGTCTCTCATTTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAAATCCA	420
1476	TCCAGTGCCTTCATTATTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAAATCCA	1417
421	GGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA	480
1416	GGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCTTTATCCCCA	1357
481	GCGAATTTGTGAATGTAAACATCATCGTTTCCATGCGGTGTTCCATTTTCAGATGGCATT	540
1356	GCGAATTTGTGAATGTAAACATCATCGTTTCCATGCGGTGTTCCATTTTCAGATGGCATT	1297
541	TTGTGTGTGTCGTTGAAGCCTTGGCCGAGCGCGGCGAGCGCTGGGCGAGCTGGGCGGAG	600
1296	TTGTGTGTGTCGTTGAAGCCTTGGCCGAGCGCGGCGAGCGCTGGGCGAGCTGGGCGGAG	1237
601	CTGACCGCGGGCGGAGAGCGAGCGCGGCGGGC	634
1236	CTGACCGCGGGCGGAGAGCGAGCGAGCGCGGCGGGC	1203

RESULT 8

AAA46679/c
 ID AAA46679 standard; cDNA; 649 BP.
 XX
 XX AAA46679;
 XX
 XX
 DT 25-SEP-2000 (first entry)
 XX
 XX
 DE cDNA of a human gene encoding cellular ligand of annexin II.

Differentially expressed human gene; cardiac disease; kidney disease; inflammatory disease; I-80; prostacyclin-stimulating factor; tsf-2; tissue specific mRNA; insulin-like growth factor binding protein 6; OSF-1; gas-1; YMP; BTG2; pre-B cell stimulating factor homologue; SDPLA; peripheral benzodiazepine receptor; annexin II cellular ligand; p11; congenital heart failure; dilated congestive cardiomyopathy; hypertrophic cardiomyopathy; restrictive cardiomyopathy; mitral valve disease; aortic valve disease; tricuspid valve disease; angina pectoris; myocardial infarction; cardiac arrhythmia; pulmonary hypertension; arterial hypertension; renovascular hypertension; arteriosclerosis; atherosclerosis; Cardiac tumour; ss.

OS Homo sapiens.

Key	Location/Qualifiers
CDS	112..405
FT	/*taq= a

XX PN WO200035473-A2.

22-JUN-2000.

15-DEC-1999: 99WO-US029941.

18-DEC-1998: 98US-0113008P.

XX
PA (SCIO-) SCIOS INC.

XX Stanton LW, White RT, Damm DL, Lewicki JA, Joly A, Schreiner GF;
 PI
 XX WFI; 2000-451904/39.
 DR P-PSDB: AAY93605.

Preventing, diagnosing and treating cardiac, kidney and inflammatory disorders using cardiac genes that are differentially expressed in PT disease states such as cardiac arrhythmia and arteriosclerosis.

Disclosure; Fig 7L; 170pp; English.
 AAA46668-79 represent differentially expressed human genes, associated with disease states and disorders. The specification describes methods preventing, diagnosing and treating cardiac, kidney and inflammatory diseases associated with inappropriate expression of differentially expressed cardiac, kidney and inflammatory genes (e.g. AAA46668-79). These genes include 1-8U, prostacyclin-stimulating factor, isf-2, tissue specific mRNA, insulin-like growth factor binding protein 6, OSF-1, gas-1, YWP, BTG2, pre-B cell stimulating factor homologue (SPDfa), peripheral benzodiazepine receptor, and cellular ligand of annexin II (p11), respectively. These diseases include congenital heart failure, dilated congestive cardiomyopathy, hypertrophic cardiomyopathy, restrictive cardiomyopathy, mitral valve disease, aortic valve disease, tricuspid valve disease, angina pectoris, myocardial infarction, cardiac arrhythmia, pulmonary hypertension, arterial hypertension, renovascular hypertension, arteriosclerosis, atherosclerosis and/or cardiac tumours
 Sequence 649 BP; 197 A; 162 C; 137 G; 153 T; 0 U; 0 Other;

Query Match 50.1%; Score 601; DB 3; Length 649;
Best Local Similarity 99.7%; Pred. No. 7.5e-142;
Matches 623; Conservative 0; Mismatches 0; Indels

Qy	1	GGAACTAAAAAGAACTTTATTTAGGGCAAGGGGATGCAAAACAATACAAAAATCAA	60
Db	649	GGAACTAAAAAGAACTTTATTTAGGGCAAGGGGATGCAAAACAATACAAAAATCAA	59
Qy	61	AAGCTTATCTGCTATTAACTTTTCTTCTCTGCTGTGCAAAATCAGAGTTAGATTTTATTT	120
Db	589	AAGCTTATCTGCTATTAACTTTTCTTCTCTGCTGTGCAAAATCAGAGTTAGATTTTATTT	530
Qy	121	TTTACATTTTGCTAAGTGTCTGATCTGCTCATGAATCTCTTCTATGGGGGAAGCTGTGGG	180
Db	529	TTTACATTTTGCTAAGTGTCTGATCTGCTCATGAATCTCTTCTATGGGGGAAGCTGTGGG	470
Qy	181	GCAGATTCCTTAAGGACGCTTTGGGCAACTCTTATCATAGGGAGGAGGAACTGCTCATTT	240
Db	469	GCAGATTCCTTAAGGACGCTTTTGGCAACTCTTATCATAGGGAGGAGGAACTGCTCATTT	411
Qy	241	TC TGCC TACTCTCTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCAATTCGATGCAATG	300
Db	410	TC TGCC TACTCTCTTTCCCTTCTGCTTTCATGTGTACTACAAAATAGTCAATTCGATGCAATG	351
Qy	301	GTGAGGCCGCGCAATTAGGGAAGAAGCTCTGGAAGGCCACTTTGGCCATCTCTACACTGG	360
Db	350	GTGAGGCCGCGCAATTAGGGAAGAAGCTCTGGAAGGCCACTTTGGCCATCTCTACACTGG	291
Qy	361	TCCAGTGCCTTCATTTATTTGTGCACGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA	420
Db	290	TCCAGTGCCTTCATTTATTTGTGCACGCCAGAGGGTCTTTTTCATTTTCCAAAAATCCA	231
Qy	421	GGGAATCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCCCTTTATCCCCA	480
Db	230	GGGAATCCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAAGTAGCCCTTTATCCCCA	171
Qy	481	GGGAATTTGTAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAATT	540
Db	170	GGGAATTTGTAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAATT	111
Qy	541	TTGTGTGTGTCGTTGAAGCCTTTGCGCCAGAGCGGGGAGCGTGGCGAGCTGGGCGAG	600
Db	110	TTGTGTGTGTCGTTGAAGCCTTTGGCCAGAGCGGGGAGCGTGGGCGAGCTGGGCGAG	52
Qy	601	CTGGACGGGGCGGAGAGGCGAGC	625
Db	51	CTGGACGGGGCGGAGAGGCGAGC	27

RESULT 9
ABN95852/C
ID ABN95852 standard: DNA: 649 BP.

Db 410 TCTGCTACTTCTTTCCCTTCTGCTTCTCATGTGTACTACAAAATAGTCAATTTGTCATGCAATG 351
Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGACTCTGGAGCCCACTTTGCCATCTCTACACTGG 360
Db 350 GTGAGGCCCGCAATTAGGGAAGAAAGACTCTGGAGCCCACTTTGCCATCTCTACACTGG 291
Qy 361 TCCAGGTCCTTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCA 420
Db 290 TCCAGGTCCTTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCA 231
Qy 421 GGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTTTTGAAGTAGCCCTTTATCCCCA 480
Db 230 GGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTTTTGAAGTAGCCCTTTATCCCCA 171
Qy 481 GCGAATTTGTAATGTAACATCATGTTTCCATGCGGTGTCCATTTGAGATGGCAAT 540
Db 170 GCGAATTTGTAATGTAACATCATGTTTCCATGCGGTGTCCATTTGAGATGGCAAT 111
Qy 541 TTGTTGTGTCCTGTTGAAGCTTTGGCCGAGCGCGCGGAGCGTGGGCGAGCTGGGCGAG 600
Db 110 TTGTTGTGTCCTGTTGAAGCTTTGGCCGAGCGCGCGGAGCGTGGGCGAGCTGGGCGAG 52
Qy 601 CTGGACGCGGGCGGAGGCGGAGC 625
Db 51 CTGGACGCGGGCGGAGGCGGAGC 27
RESULT 16
ABQ55234/c
ID ABQ55234 standard; cDNA; 663 BP.
XX AC ABQ55234;
XX AC
XX DT 22-AUG-2002 (first entry)
XX DE Human ovarian antigen HCOOI71 cDNA, SEQ ID NO:1114.
XX KW Human; ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW inflammatory condition; immune disorder; blood disorder;
KW cardiovascular disorder; respiratory disorder; neurological disorder;
KW gastrointestinal disorder; urinary system disorder; drug screening;
KW gene therapy; chromosome mapping; forensic analysis;
KW antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW antiinflammatory; gynaecological; reproductive; gene; ss.
OS Homo sapiens.
XX W0200200677-A1.
XX PN
XX PD 03-JAN-2002.
XX PF 07-JUN-2001; 2001WO-US018569.
XX PR 07-JUN-2000; 2000US-0209467P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2002-147878/19.
XX DR P-PSDB; ABP42157.
XX PT Isolated nucleic acid molecules encoding novel ovarian polypeptides,
XX PT useful in the prevention, treatment and diagnosis of cancer (e.g. ovarian
XX PT cancer), immune disorders, cardiovascular disorders and neurological
XX PT diseases.
XX PS Claim 1; SEQ ID NO 1114; 2922pp; English.
XX

CC The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC ABP43228) and to cDNAs encoding them (ABQ54131-ABQ56305), and also
CC encompasses polypeptides 90% identical and polynucleotides 95% identical
CC to the sequences of the invention. The invention additionally relates to
CC recombinant vectors and host cells comprising human ovarian antigen
CC polynucleotides, antibodies against human ovarian antigens, and the use
CC of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC treating, prognosing or preventing various ovary and/or breast-related
CC disorders. Such conditions include ovarian cancer and breast cancer, and
CC metastatic tumours of ovarian or breast origin, reproductive system
CC disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC disorders, infections (e.g., chlamydia, HIV, toxoplasmosis), and toxic
CC shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC vaginitis), immune disorders (e.g., congenital and acquired
CC immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC respiratory disorders, neurological disorders, gastrointestinal disorders
CC and urinary system disorders. Ovarian antigen polypeptides and
CC polynucleotides may also be used in screening for compounds which
CC modulate ovarian antigen expression or activity. The polynucleotides may
CC further be used for gene therapy, chromosome mapping, in the
CC identification of individuals and in forensic analysis, and the
CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents cDNA encoding a human ovarian antigen of the
CC invention. Note: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 663 BP; 213 A; 148 C; 144 G; 152 T; 0 U; 6 Other;
Query Match 49.7%; Score 595.8; DB 6; Length 663;
Best Local Similarity 99.5%; Pred. No. 1.6e-140;
Matches 597; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
Qy 2 GAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAAA 61
Db 601 GAACTAAAAAGAACTTTATTTATTGAGGGCAAGGGGATGCAACCAATNCAAAAATCAAA 542
Qy 62 AGCTTATCTGGTATTTAACTTTTCTTCTGCTGTTGTTCAATGAGAGTTAGATTTATTT 121
Db 541 AGCTTATCTGGTATTTAACTTTTCTTCTGCTGTTGTTCAATGAGAGTTAGATTTATTT 482
Qy 122 TTACATTTGCTAAGTCTCTGATCTCATGAAATCCTTCTATGCGGGAAGCTGTGGGG 181
Db 481 TTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCCTTCTATGCGGGAAGCTGTGGGG 422
Qy 182 CAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTT 241
Db 421 CAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCATTT 362
Qy 242 CTGCTTACTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTTGCGAATGG 301
Db 361 CTGCTTACTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTTGCGAATGG 302
Qy 302 TGAGGCCCGCAATTTAGGGAAGAAAGCTCTGGAGCCCACTTTGCCATCTCTACACTGGT 361
Db 301 TGAGGCCCGCAATTTAGGGAAGAAAGCTCTGGAGGCCCACTTTGCCATCTCTACACTGGT 242
Qy 362 CCAGGTCTTTTCAATTTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCAG 421
Db 241 CCAGGTCTTTTCAATTTATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAAATCCAG 182
Qy 422 GGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTTAAGTAGCCCTTTATCCCCA 481
Db 181 GGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTTAAGTAGCCCTTTATCCCCA 122
Qy 482 CGAATTTGTGAATGTAACATCATGTTTCCATGCGGTGTTCCATTTTGAGATGGCAATTT 541
Db 121 CGAATTTGTGAATGTAACATCATGTTTCCATGCGGTGTTCCATTTTGAGATGGCAATTT 62
Qy 542 TGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGCGAGCGCTGGGCGAGCTGGGCGAGC 601

PS Claim 1; SEQ ID NO 890; 147pp; English.

XX The invention relates to polynucleotides encoding colon tumour proteins.

CC The polynucleotides and encoded polypeptides are useful in pharmaceutical

CC compositions, such as vaccines, for the diagnosis, prevention, and

CC treatment of colon cancer. Polynucleotide sequences may be used as

CC hybridisation probes or primers, and in the design and preparation of

CC ribozyme molecules for inhibiting expression of tumour polypeptides and

CC proteins in tumour cells. The compositions are useful for stimulating an

CC immune response against cancer, particularly for the immunotherapy of

CC colon cancer, and as markers for the progression of cancer. ABK4450-

CC ABK46237 represent coding sequences of human colon tumour proteins of the

CC invention. Note: With the exception of SEQ ID NO 1 and 2, the sequence

CC data for this patent did not form part of the printed specification but

CC was supplied by the European Patent Office

XX

SQ Sequence 571 BP; 139 A; 115 C; 107 G; 203 T; 0 U; 7 Other;

Query Match 44.8%; Score 537; DB 6; Length 571;

Best Local Similarity 98.7%; Pred. No. 1.2e-125;

Matches 537; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

Qy 1 GGAACATAAAAGAACCTTTATTTGAGGCGAAGGGATGCAAAACAATCAAAATCAA 60

Db 28 GNAACATAAAAGAACCTTTATTTGAGGCGAAGGGATGCAAAACAATCAAAATCAA 87

Qy 61 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTCAAAATCAGAGTTAGATTTTATT 120

Db 88 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTCAAAATCAGAGTTAGATTTTATT 147

Qy 121 TTTACATTTGCTAAGTGTCTGTGCTCTCATGAAATCTTCTATGGGGGAAGCTGTGGG 180

Db 148 TTTACATTTGCTAAGTGTCTGTGCTCTCATGAAATCTTCTATGGGGGAAGCTGTGGG 207

Qy 181 GCAGATTCCTTAAGCGACCTTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAT 240

Db 208 GCANATTCCTTAAGCGACCTTTTGGGACAACTTTATCAGGGAGGAGCGAACTGCTCAT 267

Qy 241 TCTGCCCTACTCTTTCCCTCTCTGCTTCTATGTTACTACAAATAGTTCATGCAATGCAATG 300

Db 268 TCTGCCCTACTCTTTCCCTCTCTGCTTCTATGTTACTACAAATAGTTCATGCAATGCAATG 327

Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360

Db 328 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 387

Qy 361 TCCAGGTCTCTTATATTTTGTCCACAGCAGAGGGTCTTTTGTGATTTTCCAAATATCCA 420

Db 388 TCCAGGTCTCTTATATTTTGTCCACAGCAGAGGGTCTTTTGTGATTTTCCAAATATCCA 447

Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTTGTGATGAGCCCTTTATCCCCA 480

Db 448 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTTGTGATGAGCCCTTTATCCCCA 507

Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGGCAAT 540

Db 508 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGATGAGCAAT 567

Qy 541 TTGG 544

Db 568 TTGG 571

RESULT 19

AAC10823/c

ID AAC10823 standard; cDNA; 582 BP.

XX

AC

AC AAC10823;

XX

XX 06-OCT-2000 (first entry)

XX

XX Human secreted protein 5' EST, SEQ ID NO: 14898.

DE

XX

KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.

XX Homo sapiens.

OS

XX EP1033401-A2.

PN

XX 06-SEP-2000.

PD

XX 21-FEB-2000; 2000EP-00200610.

PF

XX 26-FEB-1999; 99US-0122487P.

XX

XX (GEST) GENSET.

PA

XX Dumas Milne Edwards J, Duclert A, Giordano J;

PI

XX WPI; 2000-500381/45.

DR

XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures.

PT

PT Claim 1; SEQ ID NO 14898; 71pp + Sequence Listing; English.

XX

PS The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

CC

XX

SQ Sequence 582 BP; 183 A; 135 C; 130 G; 129 T; 0 U; 5 Other;

Query Match 43.6%; Score 523; DB 3; Length 582;

Best Local Similarity 97.9%; Pred. No. 4.1e-122;

Matches 547; Conservative 4; Mismatches 4; Indels 4; Gaps 2;

Qy 30 GGCAAGGGATGCAAAACAATACAAAATCAAAAAGCTTATCTGTTATTTAACTTTCTTTC 89

Db 582 GGCAAGGGATGCAAAACAATACAAAATCAAAAAGCTTATCTGTTATTTAACTTTCTTTC 523

Qy 90 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTGCTTAAGTGCTCTGATCTGCT 149

Db 522 TCTGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTGCTTAAGTGCTCTGATCTGCT 463

Qy 150 CATGAAATCCTTCTATGGGGAGAGCTGTGGGGCAGATTCCTTAAGCGACCTTTTGGACA 209

Db 462 CATGAAATCCTTCTATGGGGAGAGCTGTGGGGCAGATTCCTTAAGCGACCTTTT--GACA 405

Qy 210 ACTCTTATCAGGGAGGAGGAACTGCTCATTTCTGCTACTCTTCTTCCCTTCTGCTTCAT 269

Db 404 ACTCTTATCAGGGAGGAGGAACTGCTCATTTCTGCTACTTCTTCTTCCCTTCTGCTTCAT 345

Qy 270 GTGTACTACAAAATAGTTCATTTGATGTCGAGCGCCGCAATTTAGGAAAAAGAGCT 329

Db 344 GTGTACTACAAAATAGTTCATTTGATGTCGAGCGCCGCAATTTAGGAAAAAGAGCT 285

Qy 330 CTGGAAGCCCACTTTGCCATCTCTACACTGGTGCAGGTCTTTCATTTATTTTGTCCACAGC 389

Db 284 CTGGAAGCCCACTTTGCCATCTCTACACTGGTGCAGGTCTTTCATTTATTTTGTCCACAGC 225

Qy 390 CAGAGGGTCTTTTGTGATTTTCCAAAATCCAGGGAATCTCTTCCATGAGTACTCTCAG 449

Db 224 CAGAGGGTCT--TTTGTATTTTCCAAAATCCAGGGAATCTCTTTCATGAGTACTCTCAG 167

QY 450 GTCCTCTTTGTTAAGTAGCCTTTATCCACGCAATTTGTGAATGTAAACATCATGGT 509
 |||||
 DB 166 GTCCTCTTTGTTAAGTAGCCTTTATYCCACGCAATTTGGAATGTAAACATCATGGT 107
 |||||
 QY 510 TTCCATGGCGTGTTCATTTGAGATGGCATTTTGGTGTGGTCCCTTGAAGCCTTTGGCCGA 569
 |||||
 DB 106 TTCCATGGCGTGTTCATTTGAGATGGCATTTTGGTGTGGTCCCTTGAAGCCTTTGGCCGA 47
 |||||
 QY 570 GGCGCGGCGACGCTGGGC 588
 |||||
 DB 46 GGCGCGGCGGCTGTGCG 28
 |||||
 RESULT 20
 ID ADK11670 standard; DNA; 530 BP.
 XX
 AC ADK11670;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Breast cancer differentially expressed gene product #76.
 XX
 KW ds; cytostatic; gene therapy; DXFzp5661133 activity inhibitor;
 KW breast cancer; differential expression.
 XX
 OS Homo sapiens.
 XX
 PN WO2003057926-A1.
 XX
 PD 17-JUL-2003.
 XX
 PF 08-JAN-2003; 2003WO-US000657.
 XX
 PR 08-JAN-2002; 2002US-0345637P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Hansen R;
 XX
 DR WPI; 2003-577534/54.
 XX
 XX Inhibiting a cancerous phenotype of a cell, useful for treating breast
 PT cancer comprises contacting a cancerous mammalian cell with an agent for
 PT inhibition of DXFzp5661133 activity.
 XX
 PS Claim 30; SEQ ID NO 76; 257pp; English.
 XX
 CC The invention relates to a method of inhibiting a cancerous phenotype of
 CC a cell comprises contacting a cancerous mammalian cell with an agent for
 CC inhibition of DXFzp5661133 activity. The methods are useful for treating
 CC cancer, e.g. breast cancer. This sequence represents a gene product which
 CC is differentially expressed in breast cancer cells. The sequence can be
 CC used in the method of the invention.
 XX
 SQ Sequence 530 BP; 160 A; 133 C; 124 G; 113 T; 0 U; 0 Other;
 Query Match 43.1%; Score 516.8; DB 10; Length 530;
 Best Local Similarity 99.6%; Pred. No. 1.5e-120;
 Matches 518; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 102 ATGAGATTAGATTTTATTTTACATTTGCTTAAGTGTCTGATCTGCTCATGAATCCTT 161
 |||||
 DB 530 ATGAGATTAGATTTTATTTTACATTTGCTTAAGTGTCTGATCTGCTCATGAATCCTT 471
 |||||
 QY 162 CTATGGGGGAAGCTGTGGGCGAGATTCCTTAAGCGACCCCTTTGGACAACCTTTATCAGG 221
 |||||
 DB 470 CTATGGGGGAAGCTGTGGGCGAGATTCCTTAAGCGACCCCTTTGGACAACCTTTATCAAG 411
 |||||
 QY 222 GAGGAGGAAGCTGCTCATTTTCTGCTACTTCTTCCCTTCTGCTTCAATGTGTACTACAA 281
 |||||
 DB 410 GAGGAGGAAGCTGCTCATTTTCTGCTACTTCTTCCCTTCTGCTTCAATGTGTACTACAA 351
 |||||

QY 282 ATAGTCATTGCAATGCTGAGGCCCGCAATTAGGAAAAAGACTCTGGAAGCCAC 341
 |||||
 DB 350 ATAGTCATTGCAATGCTGAGGCCCGCAATTAGGAAAAAGACTCTGGAAGCCAC 291
 |||||
 QY 342 TTGCGCATCTCTACATGCTGAGGCCCGCAATTAGGAAAAAGACTCTGGAAGCCAC 401
 |||||
 DB 290 TTGCGCATCTCTACATGCTGAGGCCCGCAATTAGGAAAAAGACTCTGGAAGCCAC 231
 |||||
 QY 402 TTGATTTTCCAAAAATCCAGGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCTTTGT 461
 |||||
 DB 230 TTGATTTTCCAAAAATCCAGGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCTTTGT 171
 |||||
 QY 462 TAAAGTAGCCTTTATCCCGACGCAATTTGTGAATGTAAACATCATGTTTCCATGGCGTG 521
 |||||
 DB 170 TAAAGTAGCCTTTATCCCGACGCAATTTGTGAATGTAAACATCATGTTTCCATGGCGTG 111
 |||||
 QY 522 TTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCCTTGGCCGAGCGGCGGAC 581
 |||||
 DB 110 TTCCATTTGAGATGGCATTTTGGTGTGGTCCGTTGAAGCCCTTGGCCGAGCGGCGGAC 51
 |||||
 QY 582 GCTGGGCGAGCTGGGCGAGCTGGACGCGGGCGGAGAGGC 621
 |||||
 DB 50 GCTGGGCGAGCTGGGCGAGCTGGACGCGGGCGGAGAGGC 11
 |||||
 RESULT 21
 ACC51060/c
 ID ACC51060 standard; cDNA; 2016 BP.
 XX
 AC ACC51060;
 XX
 DT 13-JUN-2003 (first entry)
 XX
 DE Human S-100A10 Related Protein coding sequence.
 XX
 KW Human; GENSET; therapeutic; therapy; gene; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200294864-A2.
 XX
 PD 28-NOV-2002.
 XX
 PF 06-AUG-2001; 2001WO-IB001715.
 XX
 PR 25-MAY-2001; 2001US-0293574P.
 PR 15-JUN-2001; 2001US-0298698P.
 PR 29-JUN-2001; 2001US-0302277P.
 PR 13-JUL-2001; 2001US-0305456P.
 XX
 PA (GEST) GENSET.
 XX
 PI Bejanin S, Tanaka H;
 XX
 DR WPI; 2003-129412/12.
 DR P-PSDB; ABR48453.
 XX
 PT New GENSET polynucleotides and polypeptides, useful for preparing a
 PT composition for treating GENSET-related disorders and as reagents in
 PT assays to quantitatively determined levels of GENSET expression in
 PT biological samples.
 XX
 PS Claim 1; Page 400-401; 505pp; English.
 XX
 CC The present invention relates to novel human GENSET coding sequences
 CC (ACC51060-ACC51115) and proteins (ABR48453-ABR48508). The GENSET
 CC sequences are useful for preparing a composition for treating GENSET-
 CC related disorders. They can also be used as markers for tissues in which
 CC the corresponding protein is preferentially expressed, as molecular
 CC weight markers on Southern gels, as chromosome markers or tags to
 CC identify chromosomes, and as reagents in assays to quantitatively
 CC determined levels of GENSET expression in biological samples

PI	Drmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LW;
XX	
DR	WPI; 2003-615964/58.
XX	
PT	New polynucleotide sequences obtained from various cDNA libraries, useful
PT	as hybridization probes, as oligomers for PCR, for chromosome and gene
PT	mapping, in the recombinant production of protein, or in generating
PT	antisense DNA or RNA.
XX	
PS	Claim 1; SEQ ID NO 21508; 44pp; English.
XX	
CC	The invention relates to an isolated polynucleotide comprising any one of
CC	38043 cDNA sequences, appearing as ACH12789-ACH50831, whose sequence was
CC	determined by the technique of SBH (sequencing by hybridisation). Also
CC	included is a purified polypeptide comprising a sequence corresponding to
CC	a reading frame of the novel polynucleotide. The nucleic acid sequences
CC	are useful in diagnostics as expressed sequence tags (EST) for
CC	identifying expressed genes or for physical mapping of the human genome,
CC	in forensics, in assessing biodiversity, or in identifying mutations
CC	responsible for genetic disorders and other traits. The nucleotide
CC	sequences are also useful as hybridisation probes, as oligomers for PCR,
CC	for chromosome and gene mapping, in the recombinant production of
CC	protein, or in generating antisense DNA or RNA. The purified polypeptide
CC	is useful for generating antibodies specific for it. The present sequence
CC	is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
CC	for this patent did not form part of the printed specification, but was
CC	obtained in electronic format directly from USPTO at
CC	seqdata.uspto.gov/sequence.html?DocID=20030073623
XX	
SQ	Sequence 477 BP; 158 A; 100 C; 109 G; 109 T; 0 U; 1 Other;
	Query Match 35.8%; Score 429.4; DB 9; Length 477;
	Best Local Similarity 99.8%; Pred. No. 1.9e-98;
	Matches 430; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY	92 TGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTGCTTAAAGTGTCTGATCTGCTCA 151
DB	477 TGCTTGTCAAATGAGAGTTAGATTTTATTTTACATTTGCTTAAAGTGTCTGATCTGCTCA 418
QY	152 TGAATCTCTTCTATGGGGGAAGCTGTGGGCGAGATTCCTTAAGCGACCTTTGGGACAAC 211
DB	417 TGAATCTCTTCTATGGGGGAAGCTGTGGGCGAGATTCCTTAAGCGACCTTTGGGACAAC 358
QY	212 TCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCTTACTTCTTCCCTTCTGCTTCATGT 271
DB	357 TCTTATCAGGGAGGAGCGAACTGCTCATTTCTGCTTACTTCTTCCCTTCTGCTTCATGT 298
QY	272 GTACTACAAAATAGTCAITTCATGCAATGGTGAGGCCCGCAATTAGGGAAGAAAGCTCT 331
DB	297 GTACTACAAAATAGTCAITTCATGCAATGGTGAGGCCCGCAATTAGGGAAGAAAGCTCT 238
QY	332 GGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTTCATTATTTTGTCCACAGCCA 391
DB	237 GGAAGCCCACTTTGCCATCTCTACACTGGTCCAGGTCCTTTCATTATTTTGTCCACAGCCA 178
QY	392 GAGGTCCTTTTTCATTTTCCAAAATCCAGGGAACCTCTTTTCCATGAGTACTCTCAGGT 451
DB	177 GAGGTCCTTTTTCATTTTCCAAAATCCAGGGAACCTCTTTTCCATGAGTACTCTCAGGT 118
QY	452 CCTCTCTTTGTTAAAGTAGCCTTTATCCCGAGCGAATTTGTGAAATGTAAACATCATGGTTT 511
DB	117 CCTCTCTTTGTTAAAGTAGCCTTTATCCCGAGCGAATTTGTGAAATGTAAACATCATGGTTT 58
QY	512 CCATGGCGTGT 522
DB	57 CCATGGCGTCT 47
	RESULT 23
	ADF79487/c
	ID ADF79487 standard; DNA; 434 BP.
XX	
AC	ADF79487;

QY 125 CATTGCTAAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGGAAGCTGTGGGCAG 184
DB 466 CATTGCTAAGTGTCTGATCTGCTCATGAATCCTTCTATGGGGGAAGCTGTGGGCAG 407
QY 185 ATTCCCTTAAGGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCATTTCTG 244
DB 406 ATTCCCTTAAGGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCATTTCTG 347
QY 245 CCTACTTCTTTCCCTCTCTGCTTCATGTGTAATAAATAGTCAATGCAATGCAATGGA 304
DB 346 CCTACTTCTTTCCCTCTCTGCTTCATGTGTAATAAATAGTCAATGCAATGGA 287
QY 305 GGCCCGCAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCA 364
DB 286 GGCCCGCAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTCCA 227
QY 365 GGTCCCTTCATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCAGGGA 424
DB 226 GGTCCCTTCATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAAATCCAGGGA 167
QY 425 ACTCCTTTTCCATGAGTACTCTCAGGTCCCTTTGTTAAGTAGAGCCCTTATCCCGGCA 484
DB 166 ACTCCTTTTCCATGAGTACTCTCAGGTCCCTTTGTTAAGTAGAGCCCTTATCCCGGCA 107
QY 485 ATTGTGAAATGTAACATCATGTGTTTCCATGGCGTGTTCATTTGAGATGGCATTTTGG 544
DB 106 ATTGTGAAATGTAACATCATGTGTTTCCATGGCGTGTTCATTTGAGATGGCATTTTGG 47
QY 545 TG 546
DB 46 TG 45

RESULT 25
AAH75092/c
ID AAF75092 standard; cDNA; 441 BP.
XX AC AAH75092;
XX AC
XX DT 10-MAY-2001 (first entry)
XX DE Human colon associated protein cDNA sequence #16.
XX DE
XX KW Human; colon; cancer; disease; ss.
XX OS Homo sapiens.
XX PN WO200112781-A1.
XX PD 22-FEB-2001.
XX PF 11-AUG-2000; 2000WO-US022157.
XX PR 13-AUG-1999; 99US-0148680P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Birse CE, Rosen CA;
XX DR WPI; 2001-147551/15.
XX DE
XX PT Nucleic acids encoding 13 human colon cancer associated polypeptides,
XX PT useful for preventing, diagnosing and/or treating e.g. cancers
XX PT (especially colon cancer), Parkinson's disease and diabetic retinopathy.
XX PS Claim 1; Page 314; 326pp; English.
XX CC The present invention relates to 13 human colon cancer-associated
XX CC proteins. These proteins and the nucleic acid encoding them may be used
XX CC in the prevention, diagnosis and treatment of diseases associated with
XX CC inappropriate colon cancer-associated protein expression
XX CC
SQ Sequence 441 BP; 158 A; 87 C; 89 G; 107 T; 0 U; 0 Other;

Query Match 34.3%; Score 411; DB 4; Length 441;
Best Local Similarity 100.0%; Pred. No. 8.5e-94;
Matches 411; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGAACATAAAAAAGAACTTTATTTATTTGAGGGCAAGGGATGCAAAACAATACAAAAAATCAA 60
DB 418 GGAACATAAAAAAGAACTTTATTTATTTGAGGGCAAGGGATGCAAAACAATACAAAAAATCAA 359
QY 61 AAGCTTATCTGGTATTAACTTTCTTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATT 120
DB 358 AAGCTTATCTGGTATTAACTTTCTTCTCTGCTTGTCAAAATGAGAGTTAGATTTTATT 299
QY 121 TTTACATTTTGTCTAAGTGTCTGATCTGCTCATCAAAATCCTTCTATGGGGGAAGCTGTGGG 180
DB 298 TTTACATTTTGTCTAAGTGTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 239
QY 181 GCAGATTTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTCTATT 240
DB 238 GCAGATTTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGTCTATT 179
QY 241 TCTGCCCTACTTCTTTCCCTTCTGCTTCTGCTGATGCTACTACAAAATAGTCATTTGCAATG 300
DB 178 TCTGCCCTACTTCTTTCCCTTCTGCTTCTGCTGATGCTACTACAAAATAGTCATTTGCAATG 119
QY 301 GTGAGCCCGCAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 360
DB 118 GTGAGCCCGCAATTAGGAAAAGAAAGCTCTGGAAGCCCACTTTGGCATCTCTACACTGG 59
QY 361 TCCAGTTCCTTCAATTAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCC 411
DB 58 TCCAGTTCCTTCAATTAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCC 8

RESULT 26
AAH35326/c
ID AAH35326 standard; cDNA; 632 BP.
XX AC AAH35326;
XX AC
XX DT 03-SEP-2001 (first entry)
XX DE Human colon cancer antigen encoding cDNA SEQ ID NO:2408.
XX DE
XX KW Human; colon cancer; colon cancer antigen; diagnosis; detection;
XX KW colorectal carcinoma; Chromosome 1; ss.
XX OS Homo sapiens.
XX PN WO200122920-A2.
XX PD 05-APR-2001.
XX PF 28-SEP-2000; 2000WO-US026524.
XX PR 29-SEP-1999; 99US-0157137P.
XX PR 03-NOV-1999; 99US-0163280P.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Ruben SM, Barash SC, Birse CE, Rosen CA;
XX PI WPI; 2001-235357/24.
XX DR P-PSDB; AAG75921.
XX DR
XX PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX PT useful for preventing, diagnosing and/or treating colorectal cancers.
XX PS Claim 1; Page 3960; 9803pp; English.
XX CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX CC cancer-associated nucleic acid molecules (N) and proteins (P), where the
XX CC proteins are collectively known as colon cancer antigens. The colon

CC cancer antigens have cytostatic activity and can be used in gene therapy
 CC and vaccine production. N and P may be used in the prevention, diagnosis
 CC and treatment of diseases associated with inappropriate P expression. For
 CC example, N and P may be used to treat disorders associated with decreased
 CC expression by rectifying mutations or deletions in a patient's genome
 CC that affect the activity of P by expressing inactive proteins or to
 CC supplement the patients own production of P. Additionally, N may be used
 CC to produce the colon cancer-associated ps, by inserting the nucleic acids
 CC into a host cell and culturing the cell to express the proteins. N and P
 CC can be used in the prevention, diagnosis and treatment of colorectal
 CC carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent
 CC sequences used in the exemplification of the present invention. N.B.
 CC Pages 666 to 682 and page 7053 of the sequence listing were missing at
 CC time of publication, meaning no sequences are present for SEQ ID NO:1027
 CC to 1052, 7921 and 7922

XX SQ Sequence 632 BP; 191 A; 139 C; 137 G; 146 T; 0 U; 19 Other;

Query Match 33.0%; Score 396.2; DB 4; Length 632;
 Best Local Similarity 95.7%; Pred. No. 5.5e-90;
 Matches 424; Conservative 0; Mismatches 16; Indels 3; Gaps 2;

Qy 1 GGAACTAAAGAACTTTATTATTGAGGCAAGGGATGCAACAAATACAAAATCAA 60
 Db 512 GGAACTAAAGAACTTTATTATTGAGGCAAGGGATGCAACCAATNCAAAAATCAA 453
 Qy 61 AAGCTTATCTGGTATTAACTTTCTTCTCTGCTGTCAAATGAGAGTTAGATTTTATT 120
 Db 452 AAGCTTATCTGGTATTAACTTTCTTCTCTGCTGTCAAATGAGAGTTAGATTTTATT 393
 Qy 121 TTTACATTTGCT-AAGTGTCTGAT--CTGCTCATGAAATCCTTCTATGGGGAGCTGT 177
 Db 392 TTTACATTTGCTNAAAGTGTCTGNTTNGGTCCNTAANTCCTTNTATGGGGNAACTGT 333
 Qy 178 GGGGAGATTCCTTAAGGACCCCTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTC 237
 Db 332 GGGGAGATTCCTTAAGGACCCCTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTC 273
 Qy 238 ATTTCTGCTACTTCTTTCCCTTCTGCTTCAATGATGTAACAAATAGTCATTCATGCA 297
 Db 272 ATTTCTGCTACTTCTTTCCCTTCTGCTTCAATGATGTAACAAATAGTCATTCATGCA 213
 Qy 298 ATGTGAGGCGCCCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 357
 Db 212 ATGTGAGGCGCCCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACAC 153
 Qy 358 TGGTCCAGGTCCTTCATTTATTTGTCACAGAGGCTCTTTTTCATTTTCCAAAAT 417
 Db 152 TGGTCCAGGTCCTTCATTTATTTGTCACAGAGGCTCTTTTTCATTTTCCAAAAT 93
 Qy 418 CCAGGGAACCTCTTTTCCATGAG 440
 Db 92 CCAGGGAACCTCTTTTCCATGAG 70

RESULT 27
 ADK11672/c
 ID ADK11672 standard; DNA; 350 BP.
 XX
 AC ADK11672;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Breast cancer differentially expressed gene product #78.
 XX
 KW ds; cytostatic; gene therapy; DKFZp566l133 activity inhibitor;
 KW breast cancer; differential expression.
 XX
 OS Homo sapiens.
 XX
 PN W02003057926-A1.
 XX
 PD 17-JUL-2003.

XX 08-JAN-2003; 2003WO-US000657.
 XX
 PR 08-JAN-2002; 2002US-0345637P.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 XX Hansen R;
 XX
 XX WPI; 2003-577534/54.
 DR
 XX
 PT Inhibiting a cancerous phenotype of a cell, useful for treating breast
 PT cancer comprises contacting a cancerous mammalian cell with an agent for
 PT inhibition of DKFZp566l133 activity.
 XX
 PS Claim 30; SEQ ID NO 78; 257pp; English.
 XX
 CC The invention relates to a method of inhibiting a cancerous phenotype of
 CC a cell comprises contacting a cancerous mammalian cell with an agent for
 CC inhibition of DKFZp566l133 activity. The methods are useful for treating
 CC cancer, e.g. breast cancer. This sequence represents a gene product which
 CC is differentially expressed in breast cancer cells. The sequence can be
 CC used in the method of the invention.
 XX
 SQ Sequence 350 BP; 96 A; 94 C; 84 G; 76 T; 0 U; 0 Other;

Query Match 29.0%; Score 347.4; DB 10; Length 350;
 Best Local Similarity 99.7%; Pred. No. 9.9e-78;
 Matches 348; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 273 TACTACAAAATAGTCATTTGTCATGCAATGTCAGGCGCCGCAATTAGGAAAAGAGCTCTG 332
 Db 350 TACTACAAAATAGTCATTTGTCATGCAATGTCAGGCGCCGCAATTAGGAAAAGAGCTCTG 291
 Qy 333 GAAGCCCACTTTGCCATCTCTACACGTCCTTCCATTTATTTTGTCCACAGCCAG 392
 Db 290 GAAGCCCACTTTGCCATCTCTACACGTCCTTCCATTTATTTTGTCCACAGCCAG 231
 Qy 393 AGGCTCTTTTGTATTTTCCAAAATCCAGGAACTCCTTTTCCATGAGTACTCTCAGGTC 452
 Db 230 AGGCTCTTTTGTATTTTCCAAAATCCAGGAACTCCTTTTCCATGAGTACTCTCAGGTC 171
 Qy 453 CTCTTTTGTAAAGTAGCTTTATCCCGAGCGAAATTTGTGAAATGTAAACATCATGTTTC 512
 Db 170 CTCTTTTGTAAAGTAGCTTTATCCCGAGCGAAATTTGTGAAATGTAAACATCATGTTTC 111
 Qy 513 CATGGCGTGTTCCTCATTTGAGATGCGATTTTGTGTGTCCTCGTTGAGCCTTGGCCGAGGC 572
 Db 110 CATGGCGTGTTCCTCATTTGAGATGCGATTTTGTGTGTCCTCGTTGAGCCTTGGCCGAGGC 51
 Qy 573 GCGGCGGACGCTGGGCGAGCTGGGCGAGCTGGACGCGGGGCGGAGAGGC 621
 Db 50 GCGGCGGACGCTGGGCGAGCTGGGCGAGCTGGACGCGGGGCGGAGAGGC 2

RESULT 28
 ABI99809/c
 ID ABI99809 standard; cDNA; 600 BP.
 XX
 AC ABI99809;
 XX
 DT 07-MAR-2002 (first entry)
 XX
 DE Mouse ischaemic condition related cDNA sequence SEQ ID NO:919.
 XX
 KW Mouse; ischaemia; compressive ischaemia; occlusive ischaemia;
 KW vasospastic ischaemia; ischaemic condition; ischaemic disease; ss.
 XX
 OS Mus musculus.
 XX
 PN W0200188188-A2.
 XX
 PD 22-NOV-2001.

XX 18-MAY-2001; 2001WO-JP004192.
 XX PF
 XX PR
 XX 18-MAY-2000; 2000JP-00145977.
 XX PA
 XX (UYNI-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX PI
 XX Iehikawa K, Asai S, Takabaashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 XX DR P-PSDB; ABB57331.
 XX
 XX Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 XX expression levels of particular genes defined in the specification or by
 XX determining the expression profile of a gene group comprising these
 XX genes.
 XX PS
 XX Claim 2; Page 2323-2324; 2690pp; English.
 XX CC
 XX The present invention describes a method for examining ischaemic
 XX conditions, comprising measuring the expression levels of particular
 XX genes (I) in a test sample or determining the expression profile of a
 XX gene group in the sample comprising genes selected from (I). The method
 XX is useful for examining the ischaemic condition (e.g. compressive
 XX ischaemia, occlusive ischaemia or vasospastic ischaemia) by measuring
 XX expression levels of particular genes (ABI99202 to ABI99912, encoding the
 XX protein sequences in ABB57020 to ABB57374) or by determining the
 XX expression profile of a gene group comprising these genes. The expression
 XX levels or expression profiles produced by these genes are used as an
 XX indicator when screening for ischaemic condition-improving drugs or
 XX therapeutics for ischaemic diseases. ABI99913 and ABI99914 represent PCR
 XX primers for a mouse ischaemic condition related sequence, which are used
 XX in the exemplification of the present invention
 XX SQ
 SQ Sequence 600 BP; 165 A; 140 C; 151 G; 144 T; 0 U; 0 Other;
 Query Match 28.7%; Score 343.6; DB 6; Length 600;
 Best Local Similarity 79.6%; Pred. No. 1.1e-76;
 Matches 476; Conservative 0; Mismatches 99; Indels 23; Gaps 5;
 QY 7 AAAAAAGAACTTTATTATTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAAAAGCTT 66
 DB 591 AAAAAAGAACTTTCTTTATTGAGGGCAATGGATGCAAAACAATATAAACTCAGAAGCTT 532
 QY 67 ATCTGGTAT---TTACTTTTCTTCTCTGCTGTCAATGAGAGTTAGATTTTATT 122
 DB 531 CTCTGCCATTGGATTAAGTTTCTCTCTCAGATTGTTGAATTTGGAGTTGATCTCATTTG 472
 QY 123 TACATTTTGCCTAAGTGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGGC 182
 DB 471 CACATTTCTTAAGGTTCTGATCTGCTCACAA-----GAAGCAGTGGGC 427
 QY 183 AGATTCTTAAAGCAACCTTTGG-GACAACTCTTATCAGGGAGAGCGAACTGCTCATTT 241
 DB 426 AGATTCTTCAAGTGACCCCGTGGTGAACACGCCACCGAGGTGGGGGTACCAAGTGTCCAGT 367
 QY 242 CTGCTACTTCTTTCCCTCTCTGCTTCTATGTGTACTACAAATAGTCAATTCATGCAATGG 301
 DB 366 TGGCCATATTCTTCCCTCTCTGCTTCTATGTGTACTACAAATAGTCAATTCATGCAATGG 307
 QY 302 TGAGGCCCGCAATATAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGT 361
 DB 306 TGAGCCCGGCACATAGTATAGAAAGCTCTGGAAGCCCACTTTGCCATCTCGGCATGGT 247
 QY 362 CCAGGTCTCTTATTTTGTCCACAGCGAGAGGTCTTTTGTATTTTCCAAAATCCAG 421
 DB 246 CCAGGTCTCTTATTTTGTCCACAGCGAGAGATCTTTTGTATTTTCCAAAATCCAG 187
 QY 422 GGAATCTCTTTCCATCAGTACTCTCAGGTCCCTCTTGTGTAAGTAGCTTTATCCCCAG 481
 DB 186 GGAATCTCCGTTCATCAGACACTCTCAGGTCCCTCTTGTGTAAGTAGCTTTATCCCCAG 127
 QY 482 CGAATTTGTGAAATGTAAACATCATGTGTTTCCATGGCGTGTTCATTTTGAGATGGCATTT 541

DB 126 CAAACCTGTGAACGTAAGCATCATGTTTCCATGGGTGCTCCATTTGGATGGCATTT 67
 QY 542 TGGTGTGGTCCGTTGAAGCTTTGG--CCGAGGGCGCGGACGCTGGGCGAGCTGGGC 597
 DB 66 TGAAG-AGTCTGTGCGAAACCTGGGCCCCGAAAGCGCAGATCTCTTGAAGAGCTGGGC 10
 RESULT 29
 ADK11671/c
 ID ADK11671 standard; DNA; 341 BP.
 XX AC
 XX ADK11671;
 XX DT
 XX 06-MAY-2004 (first entry)
 XX Breast cancer differentially expressed gene product #77.
 XX DE
 XX ds; cytostatic; gene therapy; DKFp566f1133 activity inhibitor;
 XX KW breast cancer; differential expression.
 XX OS Homo sapiens.
 XX PN WO2003057926-A1.
 XX PD 17-JUL-2003.
 XX PF 08-JAN-2003; 2003WO-US000657.
 XX PR 08-JAN-2002; 2002US-0345637P.
 XX PA (CHIR) CHIRON CORP.
 XX PI Hansen R;
 XX WPI; 2003-577534/54.
 XX Inhibiting a cancerous phenotype of a cell, useful for treating breast
 PT cancer comprises contacting a cancerous mammalian cell with an agent for
 PT inhibition of DKFp566f1133 activity.
 XX PS
 XX Claim 30; SEQ ID NO 77; 257pp; English.
 XX CC
 XX The invention relates to a method of inhibiting a cancerous phenotype of
 CC a cell comprises contacting a cancerous mammalian cell with an agent for
 CC inhibition of DKFp566f1133 activity. The methods are useful for treating
 CC cancer, e.g. breast cancer. This sequence represents a gene product which
 CC is differentially expressed in breast cancer cells. The sequence can be
 CC used in the method of the invention.
 XX SQ
 SQ Sequence 341 BP; 94 A; 94 C; 80 G; 73 T; 0 U; 0 Other;
 Query Match 28.3%; Score 339.4; DB 10; Length 341;
 Best Local Similarity 99.7%; Pred. No. 1e-75;
 Matches 340; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 281 AATAGTCATTGATGCAATGGTGGAGCCCGCAATTAGGGAAGAAGAGCTCTGGAAGCCCA 340
 DB 341 AATAGTCATTGATGCAATGGTGGAGCCCGCAATTAGGGAAGAAGAGCTCTGGAAGCCCA 282
 QY 341 CTTTGGCATCTCTACACTGCTCCAGTCTCTTCAATTTTGTCCAGCCAGAGGGTCTTT 400
 DB 281 CTTTGGCATCTCTACACTGCTCCAGTCTCTTCAATTTTGTCCAGCCAGAGGGTCTTT 222
 QY 401 TTTGATTTTCCAAAATCCAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTG 450
 DB 221 TTTGATTTTCCAAAATCCAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTG 162
 QY 461 TTAAGTAGCTTTTATCCCGAGCAATTTGTGAAATCTAAACATCATGTTTCCATGCGGT 520
 DB 161 TTAAGTAGCTTTTATCCCGAGCAATTTGTGAAATCTAAACATCATGTTTCCATGCGGT 102
 QY 521 GTTCCATTTGAGATGGCATTTTGTGTGTCGTCGTTGAAGCTTTGGCCGCGCGGA 580

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|||||
Db 101 GTTCCATTGAGTGGCATTTTGGTGTGCTGAAAGCCCTGGCCGAGCGCGCGGA 42
Qy 581 CGCTGGGCGAGTGGCGGAGCTGGACGCGGCGGCGGAGAGGC 621
Db 41 CGCTGGGCGAGTGGCGGAGCTGGACGCGGCGGCGGAGAGGC 1

RESULT 30
AAAA46561/c
ID AAA46561 standard; cdna; 600 BP.
AC AAA46561;
XX
XX
XX 25-SEP-2000 (first entry)
XX
XX cdna sequence encoding a potassium channel interactor polypeptide.
XX Potassium channel interactor; PCIP; potassium channel; epilepsy;
KW spinocerebellar ataxia; nervous system disorder; cardiovascular disorder;
KW transient outward current; ss.
XX
XX Rattus sp.
XX
XX Key Location/Qualifiers
XX CDS 52..339
XX FT /*tag= a
XX FT /product= "potassium channel interactor"
XX
XX WO200031133-A2.
XX
XX 02-JUN-2000.
XX
XX 19-NOV-1999; 99US-0027428.
XX
XX 20-NOV-1998; 98US-0109333P.
XX 25-NOV-1998; 98US-0110033P.
XX 30-NOV-1998; 98US-0110277P.
XX 23-APR-1999; 99US-00298731.
XX 09-JUL-1999; 99US-00350614.
XX 09-JUL-1999; 99US-00350874.
XX 21-SEP-1999; 99US-00399913.
XX 21-SEP-1999; 99US-00400492.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX (AMHP) AMERICAN HOME PROD CORP.
XX
XX Rhodes K, Betty M, Ling H, An W;
XX
XX WPI; 2000-400043/34.
XX P-PSDB; AAY93492.
XX
XX New polynucleotide with homology to the sequence encoding phosphate
PT channel interacting protein useful in the treatment of e.g. epilepsy and
PT spinocerebellar ataxia.
XX
XX Disclosure; Fig 32; 306pp; English.
XX
XX The present sequence encodes a potassium channel interactor protein
CC (PCIP). The PCIP polypeptides bind to a potassium channel, modulate the
CC activity of a potassium channel protein, and/or modulate a potassium
CC channel mediated activity in a cell. The polynucleotides and polypeptides
CC are useful in the treatment of epilepsy, and spinocerebellar ataxia, as
CC well as nervous system related disorders and cardiovascular disorders
CC associated with abnormal transient outward currents. They are also useful
CC for identifying compounds which can bind to and modulate the expression
CC and function of the PCIP nucleic acid molecules, and proteins
XX
XX Sequence 600 BP; 193 A; 131 C; 137 G; 139 T; 0 U; 0 Other;
SQ

Query Match 27.5%; Score 329.8; DB 3; Length 600;
Best Local Similarity 77.8%; Pred. No. 3.6e-73;
Matches 458; Conservative 0; Mismatches 107; Indels 24; Gaps 4;
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Qy 7 AAAAAAGAACTTTATTTATTTGAGGGCAAGGGGATGCAAAACAATACAAAAATCAAAAGCTT 66
Db |||||
569 AAAAAAGAACTTTCTTTATTTGAGGGCAACCGGATGCAAAACAATATAAAATCGAAAGCTC 510
Qy 67 ATCTGGTAT---TTAACTTTTCTTCTCTGCTGTGCARATGAGAGTTAGATTTTATTTT 122
Db |||||
509 CTCTGTCATTGGATTAACCTTTCTTCTGCTGTGCGAATGGAGTTGGATGTTATTG 450
Qy 123 TACATTTGCTAAGTGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAAGCTGTGGGC 182
Db |||||
449 CACATTTCTTAAGGTCCTGATCTGCTCA-----CAGNAAGCAGTGGGC 405
Qy 183 AGATTCCTTAAGGACCCCTTTTGGACAACCTCTTATCAGGAGGAGCGCAATGCTCATTTTC 242
Db |||||
404 AGATTCCTCAGTTGACCCCATGGGAGAGGACGCATCAAGGTGTGGGTACCCAGGC----T 349
Qy 243 TGCTACTTTCTTCCCTTCTGCTTCTGCTGCTACTACAAATAGTCATTGTCATGCAATGGT 302
Db |||||
348 CCAGTTGGCCTACTTCTTCTGCTTCTGCTGCTACTACAAATAGTCATTGTCATGCAATGAT 289
Qy 303 GAGGCCCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTTGCCATCTCTACACTGGTC 362
Db |||||
288 GAGCCCGCCACTAGTATAGAAAGCTCTGGAAGCCCACTTTTCCATCTCGGCACTGGTC 229
Qy 363 CAGTCTCTTCAATTATTTTGTCCACAGCCAGAGGTCCTTTTGTGATTTTCCAAAAATCCAGG 422
Db |||||
228 CAGTCTCTTCAATTATTTTGTCCACAGCCAGAGGTCCTTTTGTGATTTTCCAAAAATCCAGG 169
Qy 423 GAATCTCTTTTCCATGAGTACTCTCAGGTCCTCTTGTGTTAAGTAGCTTTATCCCGCAGC 482
Db |||||
168 GAATCTCTTTTCCATGAGCACTCTCAGGTCCTCTTGTGTTAAGTAGCTTTATCCCGCAGC 109
Qy 483 GAATTTGTGAAATGTAACATCATGTTTTCATGGCGTGTTCATTTTGAGATGCAATTTT 542
Db |||||
108 AATCTGTGAAATGTAAGCATCATGTTTTCATGGCATGCTCCATTTTGGATGSCATTTT 49
Qy 543 GGTGTGTCCTGTTGAAGCCTTGGCCGAGGCGCGCGACCGCTGGGCGAG 591
Db 48 GAG-AATCTGTTGAAACCTGGGCGCTGAGGCGCTGTCAGTCTTTTGGGAAG 1

RESULT 31
ABK72684/c
ID ABK72684 standard; cdna; 600 BP.
XX
XX AC ABK72684;
XX
XX DT 13-AUG-2002 (first entry)
XX
XX DE DNA encoding rat potassium channel interacting protein (PCIP) #13.
XX
XX KW Human; rat; mouse; monkey; potassium channel interacting protein; PCIP;
KW central nervous system disorder; epilepsy; spinocerebellar ataxia; gene;
KW cardiovascular disorder; amnesia; Alzheimer's disease; memory loss; ss;
KW affective disorder; sleep disorder; neurodegenerative disorder; stroke;
KW depression; Parkinson's disease; multiple sclerosis; migraine; angina;
KW psychiatric disorder; neurological disorder; arteriosclerosis;
KW retinosis; heart failure; idiopathic cardiomyopathy; gene therapy;
KW myocardial infarction.
XX
XX OS Rattus sp.
XX
XX PN WO200226984-A2.
XX
XX PD 04-APR-2002.
XX
XX PF 27-SEP-2001; 2001WO-US030463.
XX
XX PR 27-SEP-2000; 2000US-00670756.
XX 31-OCT-2000; 2000US-00703094.
XX
XX (MILL-) MILLENNIUM PHARM INC.
PA
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XX Rhodes K, Betty M, Ling H, An W;
 XX WPI: 2002-416482/44.
 DR P-PSDB; ABG60611.
 XX
 XX New isolated potassium channel interactor polypeptide, useful for
 PT treating central nervous system disorder, epilepsy, spinocerebellar
 PT ataxia, cardiovascular disorder, and nervous system related disorders.
 XX
 XX Example 21; Fig 32; 259pp; English.
 XX
 CC The invention relates to an isolated potassium channel interactor protein
 CC (PCIP) and the polynucleotide encoding it. The DNA and protein sequences
 CC are useful for treating potassium channel associated disorders such as
 CC central nervous system (CNS) disorders, epilepsy, spinocerebellar ataxia,
 CC cardiovascular disorders, amnesia, Alzheimer's related memory loss,
 CC affective disorders, sleep disorders, neurodegenerative disorders such as
 CC Alzheimer's disease, Parkinson's disease and multiple sclerosis,
 CC psychiatric disorders such as depression, neurological disorders such as
 CC migraine and stroke, arteriosclerosis, restenosis, heart failure, angina,
 CC idiopathic cardiomyopathy and myocardial infarction. This sequence
 CC represents cDNA encoding a PCIP of the invention
 XX
 XX Sequence 600 BP; 193 A; 131 C; 137 G; 139 T; 0 U; 0 Other;
 SQ
 Query Match 27.5%; Score 329.8; DB 6; Length 600;
 Best Local Similarity 77.8%; Pred. No. 3.6e-73;
 Matches 458; Conservative 0; Mismatches 107; Indels 24; Gaps 4;
 Qy 7 AAAAAAGAACTTTATTATTGAGGCAAGGGGATGCAAAACAATCAAAAATCAAAAGCTT 66
 Db 569 AAAAAAGAACTTTCTTTATTGAGGCAACCGATGCAAAACAATATAAACTCGAAGACTC 510
 Qy 67 ATCTGGTAT-----TTAACTTTTCTTCTGCTGTGCAAAATGAGAGTTAGATTATTTT 122
 Db 509 CTCTGTCTATGGATTAATTTCTTCTGCTGTGCAAAATGAGAGTTAGATTATTTT 450
 Qy 123 TACATTTGCTAAGTGCTCTGATCTCATGAAATCTTCTATGGGGAAGCTGTGGGC 182
 Db 449 CACATTTCTNAGGCTCTGATCTCTCA-----CAGAGAGCTGTGGGC 405
 Qy 183 AGATTCTTTAAGGACCTTTTGGACAACTTTATCAGGAGGAGCGCACTGCTCAATTC 242
 Db 404 AGATTCTCTAGTTCACCCATGGGAGGAGCGCATCAAGTGTGGTACCAGGC-----T 349
 Qy 243 TGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTTCATGTGCAATGGT 302
 Db 348 CCAGTTGGCTTACTTCTTCTGCTTCATGTGTACTACAAAATAGTTCATGTGCAATGAT 289
 Qy 303 GAGCCCGCAATTAGGGAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
 Db 288 GAGCCCGCCACTAGTGATAGAAGCTCTGGAAGCCCACTTTCCATCTCGGCACTGGTC 229
 Qy 363 CAGTCTCTTCAATTTTGTCCACAGCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 422
 Db 228 CAGTCTTTCATTTTGTCCACAGCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGG 169
 Qy 423 GAATCTCTTTTCCATAGTACTCTCAGTCTCTCTTGTGTTAAGTGGAGCTTTATCCCGAG 482
 Db 168 GAATCTCTTTTCCATAGTACTCTCAGTCTCTCTTGTGTTAAGTGGAGCTTTATCCCGAG 109
 Qy 483 GAATTTGGAATCTAATCATGTTTTCATGCGGTGTTCCATTTGAGATGCAATTT 542
 Db 108 AAACCTGGAATGTAAAGCATCATGGTTTCATGGCATGCTCCATTTGGATGCAATTT 49
 Qy 543 GGTGTGTCTTGAAGCTTTGGCCGAGCGCGCGGACGCTGGCGGAG 591
 Db 48 GAAG-AATCTGTTGAACCTGGGCGCTGAGCGCTGCGAGCTTTTGGAG 1

ID ABK63467 standard; cDNA; 573 BP.
 AC ABK63467;
 XX
 DT 18-JUN-2002 (first entry)
 XX
 DE Rat sequence differentially expressed in response to a hepatotoxin #1374.
 DE Rat; ss; hepatotoxin; expressed sequence tag; EST; drug screening;
 KW differential expression; centrilobular necrosis; steatosis.
 XX
 OS Rattus norvegicus.
 XX
 PN WO200210453-A2.
 XX
 PD 07-FEB-2002.
 XX
 PF 30-JUL-2001; 2001WO-US023872.
 XX
 PR 31-JUL-2000; 2000US-0222040P.
 PR 02-NOV-2000; 2000US-0244880P.
 PR 11-MAY-2001; 2001US-0290029P.
 PR 15-MAY-2001; 2001US-0290645P.
 PR 22-MAY-2001; 2001US-0292336P.
 PR 06-JUN-2001; 2001US-0295798P.
 PR 13-JUN-2001; 2001US-0297457P.
 PR 19-JUN-2001; 2001US-0298884P.
 PR 09-JUL-2001; 2001US-0303459P.
 XX
 XX (GENE-) GENE LOGIC INC.
 PA
 XX Mendrick D, Porter MW, Johnson KR, Castle AL, Elashoff MR;
 PI
 XX WPI: 2002-241625/29.
 DR
 XX
 XX Predicting toxic effects of compounds or the progression of these toxic
 PT effects by determining the changes in gene expression in tissues or cells
 PT exposed to the toxin and comparing these to gene expression in unexposed
 PT tissues or cells.
 XX
 PS Claim 1; SEQ ID NO 1374; 239pp; English.
 XX
 CC The invention relates to methods for predicting toxic effects of
 CC compounds or the progression of these toxic effects by determining the
 CC global changes in gene expression in tissues or cells exposed to the
 CC toxin and comparing these to gene expression in unexposed tissues or
 CC cells. Also included are methods of predicting at least one toxic effect
 CC of a compound or progression of a toxic effect, preferably the
 CC hepatotoxicity of a compound, comprising detecting the level of
 CC expression in a tissue or cell sample exposed to the compound of two or
 CC more genes listed in the specification, where differential expression of
 CC the genes is indicative of at least one toxic effect or progression. The
 CC method can also be used to identify an agent which modulates the toxic
 CC response and predict cellular pathways that a compound modulates in a
 CC cell. The methods utilise a set of at least two probes (on a solid
 CC support in kit form), where each of the probes comprises a sequence that
 CC specifically hybridises to a gene listed in the specification, a computer
 CC system comprising a database containing information identifying the
 CC expression level in a tissue or cell sample exposed to a hepatotoxin of a
 CC set of genes comprising at least two genes listed in the specification,
 CC and a user interface to view the information used to present information
 CC identifying the expression level in a tissue or cell of at least one gene
 CC listed in the specification. The method is useful for elucidating global
 CC changes in gene expression and for identifying toxicity markers in
 CC tissues or cell exposed to a known toxin. The genes may be used as
 CC toxicity markers in drug screening and toxicity assays. The genes and
 CC gene expression information may be used as diagnostic markers for the
 CC prediction or identification of the physiological state of tissue or cell
 CC sample that has been exposed to a compound or agent. Hepatotoxicity is
 CC characterised by centrilobular necrosis and steatosis. The present
 CC sequence is an expressed sequence tag (EST) or cDNA derived from a gene
 CC which is differentially expressed in response to a hepatotoxic agent
 XX

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SQ Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;
Query Match 27.5%; Score 329.2; DB 6; Length 573;
Best Local Similarity 78.2%; Pred. No. 4.9e-73;
Matches 455; Conservative 0; Mismatches 103; Indels 24; Gaps 4;
Qy 7 AAAAAGAACCTTTATTTAGGGGCAAGGGATGCAAAACATACAAAATCAAAAGCTT 66
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
563 AAAAAGAACCTTTATTTAGGGGCAAGGGATGCAAAACATACAAAATCAAAAGCTC 504
Qy 67 ATCTGGTAT---TTAACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 122
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
503 CTCTGTCTATGGATTAACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
Qy 123 TACATTTGCTAAAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
443 CACATTTCTTAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 399
Qy 183 AGATTTCTTAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 242
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
398 AGATTTCTTAAGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 343
Qy 243 TGCCTACTTCTTTCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
342 CCAGTTGGCCCTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 283
Qy 303 GAGCCCGCAATAGGGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
282 GAGCCCGCCACTAGTATAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTGCGCACTGGTC 223
Qy 363 CAGGTCTCTTCAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 422
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
222 CAGGTCTCTTCAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 163
Qy 423 GAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
162 GAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 103
Qy 483 GAACTTTGTGAATGTAAACATCATGTTTCCATGGCGGTGTTTCCATTTGAGATGCAATTTT 542
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
102 AAACCTGTGAATGTAAAGCATCATGTTTCCATGGCATGCTCCATTTGGATGGCATTTT 43

RESULT 33
ADB5858/c
ID ADB58585 standard; DNA; 573 BP.
XX
AC ADB58585;
XX
DT 04-DEC-2003 (first entry)
XX
DE Toxicity-related gene, SEQ ID 3611.
XX
KW Toxic; toxin; gene expression profile; hepatotoxicity; liver;
KW drug screening; toxicity assay; ds.
XX
OS Unidentified.
XX
PN WO2003064624-A2.
XX
PD 07-AUG-2003.
XX
PF 31-JAN-2003; 2003WO-US003194.
XX
PR 31-JAN-2002; 2002US-00060087.
PR 15-MAR-2002; 2002US-0364045P.
PR 15-MAR-2002; 2002US-0364055P.
PR 30-DEC-2002; 2002US-0436643P.
XX
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(GENE-) GENE LOGIC INC.
Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Elashoff M;
WPI; 2003-689530/65.
Predicting a toxic effect of a compound, useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays, comprises preparing gene expression profile of tissue or cells exposed to the compound.
Claim 1; SEQ ID NO 3611; 1156pp; English.
The present invention relates to a method for predicting a toxic effect of a compound. The method comprises preparing a gene expression profile of a tissue or cell sample exposed to the compound, and comparing the gene expression profile to a database comprising SEQ ID 1-4925, where differential expression of the gene indicates at least one toxic effect. The method is useful for predicting at least one toxic effect of a compound, predicting hepatotoxicity or the progression of a toxic effect of a compound, identifying an agent that modulates the onset or progression of a toxic response, predicting the cellular pathways that a compound modulates in a cell, and identifying an agent that modulates at differential expression, are useful in identifying toxicity markers in liver tissues or cells for drug screening and toxicity assays. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
SQ Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;
Query Match 27.5%; Score 329.2; DB 10; Length 573;
Best Local Similarity 78.2%; Pred. No. 4.9e-73;
Matches 455; Conservative 0; Mismatches 103; Indels 24; Gaps 4;
Qy 7 AAAAAGAACCTTTATTTAGGGGCAAGGGATGCAAAACATACAAAATCAAAAGCTT 66
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
563 AAAAAGAACCTTTATTTAGGGGCAAGGGATGCAAAACATACAAAATCAAAAGCTC 504
Qy 67 ATCTGGTAT---TTAACTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 122
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
503 CTCTGTCTATGGATTAACCTTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 444
Qy 123 TACATTTGCTAAAGTCT 182
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
443 CACATTTCTTAAGGCT 399
Qy 183 AGATTTCTTAAGGCT 242
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
398 AGATTTCTTAAGGCT 343
Qy 243 TGCCTACTTCTTTCCCT 302
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
342 CCAGTTGGCCCTACT 283
Qy 303 GAGCCCGCAATAGGGAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGGTC 362
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
282 GAGCCCGCCACTAGTATAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTGCGCACTGGTC 223
Qy 363 CAGGTCTCTTCAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 422
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
222 CAGGTCTCTTCAATTTTGTCCACAGCCAGAGGCTCTTTTGTATTTTCCAAAATCCAGG 163
Qy 423 GAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 482
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
162 GAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 103
Qy 483 GAACTTTGTGAATGTAAACATCATGTTTCCATGGCGGTGTTTCCATTTGAGATGCAATTTT 542
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
102 AAACCTGTGAATGTAAAGCATCATGTTTCCATGGCATGCTCCATTTGGATGGCATTTT 43
Qy 543 GGTGTGTCCTTGAAGCTTTGGCGGAGGCGCGCGGAGCGCT 584
Db ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
42 GAAG-AATCTGTTGAAACCTGGGCCCTGAGCGCGCTGCAGTCT 2

Qy	543	GGTGTGTCCTGTTGAACCTTGGCCGAGCGCGCGGACGCT	584
Db	42	GAAG-AATCTGTGAAACCTGGGCCCTGAGGCGCTGCAGTCT	2
XX	RESULT 34		
XX	ADB53216/c		
XX	ADB53216 standard; DNA; 573 BP.		
XX	ADB53216;		
XX	04-DEC-2003 (first entry)		
XX	Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:3758.		
XX	toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;		
XX	toxicity marker; toxicity progression; drug screening;		
XX	primary rat hepatocyte toxicity modelling; gene; ds.		
XX	Rattus norvegicus.		
XX	WO2003065993-A2.		
XX	14-AUG-2003.		
XX	04-FEB-2003; 2003WO-US003482.		
XX	04-FEB-2002; 2002US-0353171P.		
XX	13-MAR-2002; 2002US-0363534P.		
XX	08-APR-2002; 2002US-0370248P.		
XX	10-APR-2002; 2002US-0371134P.		
XX	10-APR-2002; 2002US-0371135P.		
XX	10-APR-2002; 2002US-0371150P.		
XX	11-APR-2002; 2002US-0371413P.		
XX	19-APR-2002; 2002US-0373601P.		
XX	19-APR-2002; 2002US-0373602P.		
XX	22-APR-2002; 2002US-0374139P.		
XX	08-MAY-2002; 2002US-0378370P.		
XX	09-MAY-2002; 2002US-0378652P.		
XX	09-MAY-2002; 2002US-0378653P.		
XX	09-MAY-2002; 2002US-0378665P.		
XX	09-JUL-2002; 2002US-0394230P.		
XX	09-JUL-2002; 2002US-0394253P.		
XX	04-SEP-2002; 2002US-0407688P.		
XX	28-JAN-2003; 2003US-0442900P.		
XX	(GENE-) GENE LOGIC INC.		
XX	Mendrick D, Porter M, Johnson K, Higgs B, Castle A, Orr M;		
XX	Elashoff M;		
XX	WPI; 2003-731472/69.		
XX	Determining if a compound induces a toxic effect on a tissue or cell, for		
XX	identifying hepatotoxic compounds, comprises comparing a gene expression		
XX	profile of a tissue or cell sample to a database of Tox mean and non-Tox		
XX	mean values.		
XX	Claim 44; SEQ ID NO 3758; 874pp; English.		
XX	The present invention describes a method for determining whether a		
XX	compound induces a toxic effect on a tissue or cell. The method comprises		
XX	preparing a gene expression profile of a tissue or cell sample exposed to		
XX	the compound, and comparing the gene expression profile to a database		
XX	comprising data or information on the Tox mean and non-Tox mean value.		
XX	The method is useful for predicting or identifying at least one toxic		
XX	effect, particularly hepatotoxicity, of a test or unknown compound. The		
XX	genes listed in the specification are useful as diagnostic or toxicity		
XX	markers for the prediction or identification of the physiological state		
XX	of tissue or cell sample that has been exposed to a compound, or to		
XX	identify or predict the toxic effects of a compound or an agent. These		
XX	may also be used as markers for monitoring toxicity progression or for		
XX	drug screening. The present sequence represents a primary rat hepatocyte		
CC	toxicity modelling related gene sequence from the present invention.		
XX	Sequence 573 BP; 171 A; 128 C; 137 G; 137 T; 0 U; 0 Other;		
SQ	Query Match 27.5%; Score 329.2; DB 10; Length 573;		
	Best Local Similarity 78.2%; Pred. No. 4.9e-73;		
	Matches 455; Conservative 0; Mismatches 103; Indels 24; Gaps 4;		
Qy	7	AAAAAGAACTTTATTATTAGGGCAAGGGGATGCAACAATACAAAATCAAAAGCTT	66
Db	563	AAAAAAGACTTTCTTTATTAGGGCAACGGATGCAACAATATAAACTCGAAAGCTC	504
Qy	67	ATCTGTAT-----TTAACTTTTCTCTCTGCTTGTCAAAATGAGAGTTAGATTTT	122
Db	503	CTCTGTCATGGATTAACCTTTCTCTCTGCTTGTGCAATGGAGTTGAGTGTATTG	444
Qy	123	TACATTTGCTAAGTGTCTCATCTGCTCAATAATCTTTCTATGGGGGAGCTGTGGGC	182
Db	443	CACATTTCTAAGGTCCTGATCTGCTCA-----CAGGAAGCAGTGGGC	399
Qy	183	AGATTCCTTAAGCGACCTTTGGGCAACTTTATCAGGAGGAGCGAACTGCTCATTC	242
Db	398	AGATTCCTCAGTTGACCCCATGGGAGGAGCGCATCAAGGTGTGGGTACCAAGGC	343
Qy	243	TGCTACTTTCTTCCCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT	302
Db	342	CCAGTTGGGCTACTTCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT	283
Qy	303	GAGGCCGCAATTAGGGAAGAAAGCTCTGGAAGCCACTTTGGCCATCTTACACATGG	362
Db	282	GAGCCCGCCACTAGTAGATAAGAAAGCTCTGGAAGCCACTTTTCCATCTCGGAC	223
Qy	363	CAGGTCTTCATTTATTTTGTCCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAT	422
Db	222	CAGGTCTTTTCAATTTTGTCCACAGCCAGAGGCTCTTTTGTGATTTTCCAAAAT	163
Qy	423	GAATCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTGATTTTCCAAAAT	482
Db	162	GAATCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGTGATTTTCCAAAAT	103
Qy	483	GAATTTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCATTTT	542
Db	102	AAACCTGTGAAATGTAAGCATCATGTTTCCATGGCATGCTCCATTTGGGATGGCAT	43
Qy	543	GGTGTGTCCTGTTGAAGCTTGGCCGAGGCGGCGGCGGCGCT	584
Db	42	GAAG-AATCTGTGAAACCTTGGGCCCTGAGGCGCTGCAGTCT	2
XX	RESULT 35		
XX	ABT42181/c		
XX	ID ABT42181 standard; DNA; 573 BP.		
XX	ABT42181;		
XX	AC		
XX	DT 26-JUN-2003 (first entry)		
XX	Toxicity modelling related rat gene SEQ ID No 1883.		
XX	Toxic effect; gene expression profile; renal toxicity; toxicity marker;		
XX	database; drug screening; toxicity assay; rat; ds.		
XX	Rattus norvegicus.		
XX	WO200295000-A2.		
XX	28-NOV-2002.		
XX	22-MAY-2002; 2002WO-US016173.		
XX	22-MAY-2001; 2001US-0292335P.		
XX	13-JUN-2001; 2001US-0297523P.		
XX	19-JUN-2001; 2001US-0298925P.		

XX WPI; 2000-673510/66.
 DR P-PSDB; AAB45540.
 XX
 XX Composition containing S100 protein, corresponding nucleic acid or
 PT vector, useful for treating cardiomyopathy and cardiac insufficiency.
 XX
 XX
 XX Claim 36; Page 17; 36pp; German.
 XX
 XX This invention describes a novel composition for treating primary or
 CC secondary cardiomyopathy or cardiac insufficiency contains at least one
 CC S100 protein (I) or nucleic acid (II) encoding (I), or their mutants or
 CC fragments, or a gene transfer vector containing (II), optionally
 CC formulated with auxiliaries and/or carriers. (II) are calcium-binding
 CC proteins involved in calcium homeostasis, so their overexpression in
 CC cardiac muscle will improve pumping capacity (and overall capacity) of
 CC the heart. In cultured myocardial cells they increase the contraction and
 CC relaxation rates associated with increased systolic calcium ion release
 CC from the sarcoplasmic reticulum (SR) and calcium re-uptake by SR. (I) are
 CC used to treat cardiomyopathy (CMP) where inherited or caused by
 CC spontaneous mutations and ischemic CMP caused by arteriosclerosis,
 CC dilative CMP caused by toxic/infectious disease, cardiac disease caused
 CC by pulmonary and/or arterial hypertension, and structural disease caused
 CC by rhythm disorders or valve defects, generally any condition associated
 CC with reduced contractile force. Unlike calmodulin, which is expressed
 CC ubiquitously, (I) show tissue-specific expression and treat the
 CC underlying defect in the sarcoplasmic reticulum (SR) that causes cardiac
 CC disease
 XX
 XX Sequence 294 BP; 96 A; 57 C; 72 G; 69 T; 0 U; 0 Other;
 SQ
 Query Match 24.5%; Score 294; DB 3; Length 294;
 Best Local Similarity 100.0%; Pred. No. 3.1e-64;
 Matches 294; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 246 CTACTCTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTCATCAATGGTGAG 305
 DB CTACTCTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTCATCAATGGTGAG 235
 QY 306 GCCCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTACACTGGTCCAG 365
 DB 234 GCCCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTACACTGGTCCAG 175
 QY 366 GTCCTTCATTATTATTGTCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAA 425
 DB 174 GTCTTCATTATTATTGTCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCCAGGGAA 115
 QY 426 CTCCTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTCCAAAATCCAGGGAA 485
 DB 114 CTCCTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTCCAAAATCCAGGGAA 55
 QY 486 TTTGTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTGAGATGGCAT 539
 DB 54 TTTGTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTGAGATGGCAT 1
 RESULT 40
 ADA08452
 ID ADA08452 standard; DNA; 291 BP.
 XX
 AC ADA08452;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX Mammalian annexin II p11 subunit antisense polynucleotide.
 DE
 XX Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
 KW plasmin reductase; reduced plasmin protein; anti-angiogenesis activator;
 KW urokinase-type plasminogen activator; A61; annexin II heterotetramer;
 KW annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
 KW protein disulphide isomerase; modulating angiogenesis; mammalian; ss.
 XX
 OS Mammalia.

XX US2003083234-A1.
 PN
 XX
 PD 01-MAY-2003.
 XX
 XX 26-NOV-2002; 2002US-00304287.
 PF
 XX
 XX 28-NOV-2001; 2001US-0333866P.
 PR
 XX
 XX (WAIS/) WAISMAN D.
 PA (KWON/) KWON M.
 PA
 XX
 XX Waisman D, Kwon M;
 PI
 XX
 XX WPI; 2003-596985/56.
 DR
 XX
 XX Producing an anti-angiogenesis plasmin fragment, useful for modulating,
 PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
 PT plasminogen polypeptide with a plasminogen activator and a plasmin
 PT reductase.
 PT
 XX
 XX Claim 33; Page 12; 29pp; English.
 PS
 XX The present invention relates to a method for producing an anti-
 CC angiogenesis plasmin fragment. The method comprises contacting a
 CC plasminogen polypeptide with a plasminogen activator and a plasmin
 CC reductase, where a reduced plasmin protein is produced and the anti-
 CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
 CC released from the reduced plasmin protein. The plasminogen activator is
 CC preferably a urokinase-type plasminogen activator. The angiogenesis
 CC plasmin fragment is A61. The plasmin reductase is selected from annexin
 CC II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
 CC disulphide isomerase. The annexin II heterotetramer is associated with a
 CC cell membrane. The method of the invention is useful for modulating (e.g.
 CC promoting or inhibiting) angiogenesis. The present sequence represents
 CC mammalian annexin II p11 subunit antisense polynucleotide.
 XX
 XX Sequence 291 BP; 68 A; 71 C; 57 G; 95 T; 0 U; 0 Other;
 SQ
 Query Match 24.3%; Score 291; DB 9; Length 291;
 Best Local Similarity 100.0%; Pred. No. 1.8e-63;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 249 CTTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTCATCAATGGTGAGGCC 308
 DB 1 CTTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTGTCATCAATGGTGAGGCC 60
 QY 309 CGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACATGTTGCCAGGTC 368
 DB 61 CGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGTTCCAGGTC 120
 QY 369 CTTTCATTATTGTTGCCACAGCCAGAGGCTCTTTTGCATTTTCCAAAATCCAGGGAACTC 428
 DB 121 CTTTCATTATTGTTGCCACAGCCAGAGGCTCTTTTGCATTTTCCAAAATCCAGGGAACTC 180
 QY 429 CTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTCCAAAATCCAGGAACTT 488
 DB 181 CTTTTCATGAGTACTCTCAGGTCCTCTTTTGTATTTTCCAAAATCCAGGAACTT 240
 QY 489 GTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTGAGATGGCAT 539
 DB 241 GTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTGAGATGGCAT 291
 RESULT 41
 ADA08453/c
 ID ADA08453 standard; DNA; 291 BP.
 XX
 AC ADA08453;
 XX
 DT 06-NOV-2003 (first entry)
 XX
 XX Mammalian annexin II p11 subunit sense polynucleotide.
 DE

XX Anti-angiogenesis plasmin fragment; plasminogen; plasminogen activator;
KW plasmin reductase; reduced plasmin protein; anti-angiogenesis activator;
KW urokinase-type plasminogen activator; A61; annexin II heterotetramer;
KW annexin II p36 subunit; annexin II p11 subunit; thioredoxin;
KW protein disulphide isomerase; modulating angiogenesis; mammalian; ss.
OS Mammalia.
XX
XX US2003083234-A1.
XX
XX 01-MAY-2003.
XX
XX 26-NOV-2002; 2002US-00304287.
XX
XX 28-NOV-2001; 2001US-0333866P.
XX (WAIS/) WAISMAN D.
XX (KWON/) KWON M.
XX
XX Waisman D, Kwon M;
XX WPI; 2003-596985/56.
XX
XX Producing an anti-angiogenesis plasmin fragment, useful for modulating,
PT e.g. promoting or inhibiting angiogenesis, comprises contacting a
PT plasminogen polypeptide with a plasminogen activator and a plasmin
PT reductase.
XX
XX Claim 41; Page 12; 29pp; English.

XX The present invention relates to a method for producing an anti-
CC angiogenesis plasmin fragment. The method comprises contacting a
CC plasminogen polypeptide with a plasminogen activator and a plasmin
CC reductase, where a reduced plasmin protein is produced and the anti-
CC angiogenesis plasmin fragment having anti-angiogenesis activity, is
CC released from the reduced plasmin protein. The plasminogen activator is
CC preferably a urokinase-type plasminogen activator. The angiogenesis
CC plasmin fragment is A61. The plasmin reductase is selected from annexin
CC II heterotetramer, annexin II p36 subunit, p11, thioredoxin, and protein
CC disulphide isomerase. The annexin II heterotetramer is associated with a
CC cell membrane. The method of the invention is useful for modulating (e.g.
CC promoting or inhibiting) angiogenesis. The present sequence represents
CC mammalian annexin II p11 subunit sense polynucleotide.

XX SQ Sequence 291 BP; 95 A; 57 C; 71 G; 68 T; 0 U; 0 Other;

Query Match 24.3%; Score 291; DB 9; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.8e-63;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 249 CTTCTTTCCCTTCCTTCATGTGTACTACAAAATAGTCATGTGCAATGGTGAGGCC 308
Db 291 CTTCTTTCCCTTCCTTCATGTGTACTACAAAATAGTCATGTGCAATGGTGAGGCC 232
Qy 309 CGCAATTAGGAAAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTCCAGGTC 368
Db 231 CGCAATTAGGAAAAGAGCTCTGGAAGCCACCTTTGCCATCTCTACACTGGTCCAGGTC 172
Qy 369 CTTCAATTAATTTTGTCCACAGCAGAGGCTCTTTTGATTTTCCAAAATCCAGGGAATC 428
Db 171 CTTCAATTAATTTTGTCCACAGCAGAGGCTCTTTTGATTTTCCAAAATCCAGGGAATC 112
Qy 429 CTTTTCATAGTACTCTCAGGTCTCTTCTTGTGTAAGTAGCTTTATCCCCAGCAATTT 488
Db 111 CTTTTCATAGTACTCTCAGGTCTCTTCTTGTGTAAGTAGCTTTATCCCCAGCAATTT 52
Qy 489 GTGAAATGAACATCATGGTTTCCATGCGCGTGTTCATTTGAGATGSCAT 539
Db 51 GTGAAATGAACATCATGGTTTCCATGCGCGTGTTCATTTGAGATGSCAT 1

ADP67424
ID ADP67424 standard; cDNA; 291 BP.
XX
XX ADP67424;
XX
XX 23-SEP-2004 (first entry)
XX
XX Human p11 antisense polynucleotide SEQ ID NO:5.
DE
XX p11; p11 activity modulator; plasminogen activation; cytostatic;
KW antisense therapy; cancer; tumour; tumour growth inhibition; antisense;
KW gene; ss; human.
XX
XX Homo sapiens.
OS
XX WO2004054517-A2.
XX
XX 01-JUL-2004.
XX
XX 12-DEC-2003; 2003WO-US040029.
XX
XX 13-DEC-2002; 2002US-0433140P.
XX
XX (MEDI-) MEDIMOMICS LLC.
XX (WAIS/) WAISMAN D.
XX
XX Waisman D;
XX
XX WPI; 2004-487995/46.
XX
XX Composition useful for inhibiting growth of tumor in patient, modulates
PT activity of p11 protein and effects change in level of plasminogen
PT activation by a cell.
XX
XX Disclosure; SEQ ID NO 5; 140pp; English.
XX
XX The present invention describes a composition (I) which modulates the
CC activity of a p11 protein and effects a change in the level of
CC plasminogen activation by a cell. Also described: (1) making (M1) a
CC clonal cell line, which involves isolating a cell, then characterising
CC the activity of a protein produced by the cell or clonal progeny of the
CC cell, where the protein is involved in plasminogen activation; and (2) a
CC clonal cell line (II) useful in the identification of composition that
CC modulate p11 activity, where the clonal cell line is obtained by (M1).
CC (I) has cytostatic activity, and can be used in antisense therapy. (I) is
CC useful for modulating the activity of p11 which involves administering
CC (I) to a cell. The cell can be a human cancer cell, chosen from a HT1080
CC fibrosarcoma cell, a LNCaP prostate cancer cell and a CCL-22 colorectal
CC adenocarcinoma cell. (I) is also useful for reducing the development of
CC cancer in a patient e.g., mouse which involves administering (I) to a
CC cancer cell in the patient. (I) is useful for inhibiting the growth of
CC tumours or inhibiting tumour cell invasion in a patient, which involves
CC administering (I) to a cancer cell in the patient. (II) is useful for
CC identifying a composition that modulates p11 activity which involves
CC administering the composition to (II) obtained by (M1), determining the
CC change in p11 activity of a cell of the clonal cell line relative to a
CC cell of a clonal cell line that had not received the composition, and
CC identifying the composition that produces a change in p11 activity. The
CC change in p11 activity is a change in the level of plasminogen activation
CC activity. The present sequence represents a human p11 antisense
CC polynucleotide sequence [antisense to ADP67425], which is used in the
CC exemplification of the present invention.

SQ Sequence 291 BP; 68 A; 71 C; 57 G; 95 T; 0 U; 0 Other;

Query Match 24.3%; Score 291; DB 12; Length 291;
Best Local Similarity 100.0%; Pred. No. 1.8e-63;
Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 249 CTTCTTTCCCTTCCTTCATGTGTACTACAAAATAGTCATGTGCAATGGTGAGGCC 308
Db 1 CTTCTTTCCCTTCCTTCATGTGTACTACAAAATAGTCATGTGCAATGGTGAGGCC 60

QY 309 CGCAATTAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTCCAGGTC 368
 Db 61 CGCAATTAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTCCAGGTC 120
 QY 369 CTTCAATTATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAAATCCAGGAACTC 428
 Db 121 CTTCAATTATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAAATCCAGGAACTC 180
 QY 429 CTTTTCATGAGTACTCTCAGGTCCTCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 488
 Db 181 CTTTTCATGAGTACTCTCAGGTCCTCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 240
 QY 489 GTGAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAT 539
 Db 241 GTGAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAT 291

RESULT 43
 ADP67425/c
 ID ADP67425 standard; cDNA; 291 BP.
 XX
 AC ADP67425;
 XX
 DT 23-SEP-2004 (first entry)
 XX
 DE Human p11 sense polynucleotide SEQ ID NO:6.
 XX
 KW p11; p11 activity modulator; plasminogen activation; cytostatic;
 KW antisense therapy; cancer; tumour; tumour growth inhibition; gene; ss;
 KW human.
 XX
 OS Homo sapiens.

XX
 XX
 FH Key Location/Qualifiers
 FT CDS 1..291
 FT /*tag= a
 FT /product= "p11"
 XX
 PN WO2004054517-A2.
 XX
 PD 01-JUL-2004.
 XX
 PF 12-DEC-2003; 2003WO-US040029.
 XX
 PR 13-DEC-2002; 2002US-0433140P.
 XX
 PA (MEDI-) MEDIOMICS LLC.
 PA (WAIS/) WAISMAN D.
 XX
 PI Waisman D;
 XX
 DR WPI; 2004-487995/46.
 DR P-PSDB; ADP67422.
 XX

Composition useful for inhibiting growth of tumor in patient, modulates activity of p11 protein and effects change in level of plasminogen activation by a cell.
 PS Disclosure; SEQ ID NO 6; 140pp; English.
 XX
 CC The present invention describes a composition (I) which modulates the activity of a p11 protein and effects a change in the level of plasminogen activation by a cell. Also described: (i) making (M1) a clonal cell line, which involves isolating a cell, then characterising the activity of a protein produced by the cell or clonal progeny of the cell, where the protein is involved in plasminogen activation; and (2) a clonal cell line (II) useful in the identification of composition that modulate p11 activity, where the clonal cell line is obtained by (M1). (I) has cytostatic activity, and can be used in antisense therapy. (I) is useful for modulating the activity of p11 which involves administering (I) to a cell. The cell can be a human cancer cell, chosen from a HRI080 fibrosarcoma cell, a lNCap prostate cancer cell and a CCL-22 colorectal adenocarcinoma cell. (I) is also useful for reducing the development of

CC cancer in a patient e.g., mouse which involves administering (I) to a cancer cell in the patient. (I) is useful for inhibiting the growth of tumours or inhibiting tumour cell invasion in a patient, which involves administering (I) to a cancer cell in the patient. (II) is useful for identifying a composition that modulates p11 activity which involves administering the composition to (II) obtained by (M1), determining the change in p11 activity of a cell of the clonal cell line relative to a cell of a clonal cell line that had not received the composition, and CC identifying the composition that produces a change in p11 activity. The change in p11 activity is a change in the level of plasminogen activation activity. The present sequence represents a human p11 sense polynucleotide sequence, which is used in the exemplification of the CC present invention.
 XX
 SQ Sequence 291 BP; 95 A; 57 C; 71 G; 68 T; 0 U; 0 Other;

Query Match 24.3%; Score 291; DB 12; Length 291;
 Best Local Similarity 100.0%; Pred. No. 1.8e-63;
 Matches 291; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 249 CTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTCATGCAATGGTGGGCC 308
 Db 291 CTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCATTCATGCAATGGTGGGCC 232
 QY 309 CGCAATTAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTCCAGGTC 368
 Db 231 CGCAATTAGGAAAGAGCTCTGGAAGCCACATTTGCCATCTCTACACTGGTCCAGGTC 172
 QY 369 CTTCAATTATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAAATCCAGGAACTC 428
 Db 171 CTTCAATTATTTTGTCCACAGCAGAGGCTCTTTTGTGATTTTCCAAAATCCAGGAACTC 112
 QY 429 CTTTTCATGAGTACTCTCAGGTCCTCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 488
 Db 111 CTTTTCATGAGTACTCTCAGGTCCTCTTTGTTAAGTAGCCTTTATCCCCAGCGAATTT 52
 QY 489 GTGAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAT 539
 Db 51 GTGAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAT 1

RESULT 44
 AAI10124
 ID AAI10124 standard; DNA; 464 BP.
 XX
 AC AAI10124;
 XX
 DT 12-OCT-2001 (first entry)
 XX
 DE Probe #57 for gene expression analysis in human cervical cell sample.
 XX
 KW Probe; human; microarray; gene expression; cervical epithelial cell;
 KW cervical cancer; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200157278-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000670.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 XX (MOLE-) MOLECULAR DYNAMICS INC.
 PA Penn SG, Hanzel DK, Chen W, Rank DR;
 XX PI

Job time : 684 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: August 17, 2005, 23:46:33 ; Search time 3771 Seconds
(without alignments)
12102.641 Million cell updates/sec

Title: US-10-735-577-16

Perfect score: 1199
Sequence: 1 ggaactaaaagaacttta.....cgggcttcgcccccaccgg 1199

Scoring table: IDENTITY NUC

Gapop 10*0 , Gapext 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*

1: gb_est1:*
2: gb_est2:*
3: gb_hc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	694.8	57.9	753	4	BI827113
C 2	688.2	57.4	769	4	BG437145
C 3	687	57.3	883	6	CD389775
C 4	668	55.7	679	4	BM785208
C 5	665	55.5	681	5	BUS21490
C 6	663	55.3	671	4	BG774775
C 7	658.8	54.9	912	2	BE729901
C 8	657	54.8	660	3	CR610742
C 9	657	54.8	660	5	BX362846
C 10	652.8	54.4	705	6	CD177393
C 11	652	54.4	670	5	BQ646470
C 12	651.6	54.3	737	4	BG339527
C 13	648	54.0	663	4	BM541317
C 14	646.6	53.9	843	5	BUS94774
C 15	646.4	53.9	669	5	BUI183451
C 16	646.4	53.9	940	5	BQ678300
C 17	645	53.8	681	4	BG332809
C 18	644	53.7	692	5	BUS02376
C 19	640.6	53.4	807	5	BUS02356
C 20	638	53.2	655	5	BQ073203
C 21	636.2	53.1	1125	4	BM549820
C 22	634.4	52.9	657	4	BI825167
C 23	634	52.9	645	2	BE378444
C 24	632	52.7	655	5	BQ050753

c	25	631.4	52.7	856	4	BG335520
c	26	630.8	52.6	666	6	CA431436
c	27	629	52.5	687	4	BM546362
c	28	628.6	52.4	938	2	BF686811
c	29	628.6	52.4	990	2	BE745512
c	30	628.4	52.4	674	4	BI858258
c	31	628.2	52.4	686	6	CA307888
c	32	627.8	52.4	811	4	BI488419
c	33	627	52.3	665	6	CA412335
c	34	626.4	52.2	641	1	AI749536
c	35	625	52.1	641	5	BQ948995
c	36	625	52.1	697	4	BI093074
c	37	622.8	51.9	637	7	CN271600
c	38	621.8	51.9	625	4	BM767559
c	39	621.4	51.8	628	4	BM842132
c	40	621	51.8	794	5	BU860855
c	41	620	51.7	638	5	BQ943717
c	42	620	51.7	898	4	BM461859
c	43	619.8	51.7	645	4	BG335338
c	44	619.4	51.7	662	5	BU934696
c	45	619	51.6	619	6	CB158822

ALIGNMENTS

RESULT 1
BI827113/c
LOCUS BI827113 753 bp mRNA linear EST 04-OCT-2001
DEFINITION 603077308F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5169265 5', mRNA sequence.
ACCESSION BI827113
VERSION BI827113.1 GI:15938663
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 753)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-rc@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM11420 row: p column: 02
High quality sequence stop: 753.
Location/Qualifiers
1. 753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5169265"
/tissue_type="medulla"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

FEATURES

source
1. 753
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5169265"
/tissue_type="medulla"
/lab_host="DH10B"
/notes="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN

Query Match		57.9%;	Score 694.8;	DB 4;	Length 753;
Best Local Similarity		98.5%;	Pred. No. 5.1e-159;		
Matches 743;		Conservative	0;	Mismatches 7;	Indels 4;
				Gaps	4;
Qy	449	GGTCCTCTTTGTTAAAGTAGCCTTTATCCCGAGCAATTTGT-CAAAATGTAAACATCATG	507		
Db	753	GGTCCTCTTTGTTAAAGTAGCCTTTATCCCGAGCGCATTTGTGGAATGTACACATCATG	694		
Qy	508	GTTT-CCATGCGCGTTCCATTTTCAGATGGCATTTTGTGTGTCCTTGAAGCCTTTGGC	566		
Db	693	GTTTCCCATGCGGTGTTCCATTTGAGATGGCATTTTGTGTGTCCTTGAAGCCTTTGTC	634		
Qy	567	CGAGCGCGCGGACGCTGGCGAGCTGGCGAGCTGAGACGCGGGCGGAGAG-GCAGAGC	625		
Db	633	CGAGCGCTCGCGGACGCTGGCGAGCTGGCGAGCTGAGACGCGGTTCGAGAGTCCGAGC	574		
Qy	626	CGCGCGGGCTGTGCGCTTCTTATAGTAGTGTGCGCGGGTGGGTAGAGAGGCGGCGGG	685		
Db	573	CGCGCGGGCTGTGCGCTTCTTATAGTAGTGTGCGCGGGTGGGTAGAGAGGGA-GCGGTGCGG	515		
Qy	686	GAGCGGGAGGAGCTGGCGGCGCTCGGCGAGGCGCTCCCGACGCGCTGTCTCTCCCGCC	745		
Db	514	GAGCGGGAGGAGCTGGCGGCGCTCGGCGAGGCGCTCCCGACGCGCTGTCTCTCCCGCC	455		
Qy	746	TCCTCTGCCCCGACTCCCGGACCCCGGCGCGGCGCCACCGCCCTGCGCTCCC	805		
Db	454	TCCTCTGCCCCGACTCCCGGACCCCGGCGCGGCGCCACCGCCCTGCGCTCCC	395		
Qy	806	GGACCCGCTCGAGAGGCTTCGCGCGCCCGCCAGACAGAGCGTTCTGTAACTTCTCTTC	865		
Db	394	GGACCCGCTCGAGAGGCTTCGCGCGCCCGCCAGACAGAGCGTTCTGTAACTTCTCTTC	335		
Qy	866	AGTAGAACGCTGCTCTCGAATATTCAGGCGATCCCGACCGCTGAGCTGCGCTTCC	925		
Db	334	AGTAGAACGCTGCTGCTCTCGAATATTCAGGCGATCCCGACCGCTGAGCTGCGCTTCC	275		
Qy	926	TCTCGGGTTTGGTTTAAAGTGTACAAATCAAGAACCCGCGCTCCTGCGGGTGGG	985		
Db	274	TCTCGGGTTTGGTTTAAAGTGTACAAATCAAGAACCCGCGCTCCTGCGGGTGGG	215		
Qy	986	CACGCTCGCGCAGAACACAGAGTAAACCGCTCTCGCGCACCTACGGGTCTAGGAATTAC	1045		
Db	214	CACGCTCGCGCAGAACACAGAGTAAACCGCTCTCGCGCACCTACGGGTCTAGGAATTAC	155		
Qy	1046	TTGCTGATGATACCTCGAGGAGTGGCAGGTGGAGTCTCTATCGACCTCAGAGGCACATC	1105		
Db	154	TTGCTGATGATACCTCGAGGAGTGGCAGGTGGAGTCTCTATCGACCTCAGAGGCACATC	95		
Qy	1106	AGATTAGCCCTAGGAGTCCGTCTGGGGTCTCGCGCGCTGCGCCAGTGGAGGGCGGC	1165		
Db	94	AGATTAGCCCTAGGAGTCCGTCTGGGGTCTCGCGCGCTGCGCCAGTGGAGGGCGGC	35		
Qy	1166	ACCTCCCGAGAGCGGGCTTCCGCGCCACCGG	1199		
Db	34	ACCTCCCGAGAGCGGGCTTCCGCGCCACCGG	1		

RESULT 2
BG437145/c
LOCUS BG437145 769 bp mRNA linear EST 14-MAR-2001
DEFINITION 602488791P1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4620694 5',
mRNA sequence.
ACCESSION BG437145
VERSION BG437145.1 GI:13343651
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 769)
NIH-MGC <http://mgi.nci.nih.gov/>.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE Unpublished (1999)
JOURNAL

COMMENT

Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: DCTD/FTP/Gazdar
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
<http://image.llnl.gov>
Plate: LNCM382 row: f column: 23
High quality sequence stop: 750.

FEATURES

source

1..769
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4620694"
/tissue_type="large cell carcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_18"
/notes="Organ: lung; Vector: pOTB7; Site: 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN

Query Match		57.4%;	Score 688.2;	DB 4;	Length 769;
Best Local Similarity		97.7%;	Pred. No. 2.1e-157;		
Matches 729;		Conservative	0;	Mismatches 14;	Indels 3;
				Gaps	3;
Qy	9	AAAAGAACTTTATTTATGAGGCAAGGGATGCAACAATACAAAAATCAAAAGCTTAT	68		
Db	746	AAAAGAACTTTATTTATTGAGGCAAGGGATGCAACAATACAAAAATCAAAAGCTTAT	687		
Qy	69	CTCGTATTTAACTTTTC-TTTCTCTGCTGTCAAAATGAGAGTTAGATTTAT-TTTTACA	126		
Db	686	CTCGTATTTAACTTTTCGTTTCTGCTGTCCAAATGAGAGTTAGATTTATTTGTTGACA	627		
Qy	127	TTTGTCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAAGCTGTGGGGCAGAT	186		
Db	626	TTTGTCTAAGTGTCCTGATCTGCTCATGAAATCCTTCTATGGGGAAAGCTGTGGGGCAGAT	567		
Qy	187	TCCTTAAGCGACCTTTGGGAGAACTTTATCAGGGAGGAGCGAACTGCTCATTTCTGCC	246		
Db	566	TCCTTAAGCGACCTTTGGGAGAACTTTATCAGGGAGGAGCGAACTGCTCATTTCTGCC	507		
Qy	247	TACTTCTTTCCCTTCTGCTTCTATGTACTTACAAAATAGTCAATTGCAATGCAATGGTGAGG	306		
Db	506	TACTTCTTTCCCTTCTGCTTCTATGTACTTACAAAATAGTCAATTGCAATGCAATGGTGAGG	447		
Qy	307	CCCGCAATTAGGGAAAGAGCTCTGGAAAGCCCACTTTGCCATCTCTTACATCGGTCCAGG	366		
Db	446	CCCGCAATTAGGGAAAGAGCTCTGGAAAGCCCACTTTGCCATCTCTTACATCGGTCCAGG	387		
Qy	367	TCC-TTCATTTATTTGTCCACGCCAGAGGTCTTTTGTGATTTTCCAAAATCCAGGGAA	425		
Db	386	TCGGTTCATTTATTTGTCCACGCCAGAGGGTCTTTTGTGATTTTCCAAAATCCAGGGAA	327		
Qy	426	CTCCTTTTCCATGAGTACTCTCAGGTCCCTCTTTGTTAGTAGCCTTTATCCCCAGCGAA	485		
Db	326	CTCCTTTTCCATGAGTACTCTCAGGTCCCTCTTTGTTAGTAGCCTTTATCCCCAGCGAA	267		
Qy	486	TTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCATTTTGGT	545		
Db	266	TTTGTGAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCATTTTGGT	207		
Qy	546	GTGGTCGTTGAAGCCTTGGCCGAGGGCGGCGAGCTGGGGGAGCTGGGGCAGCTGGA	605		
Db	206	GTGGTCGTTGAAGCCTTGGCCGAGGGCGGCGAGCTGGGGGAGCTGGGGCAGCTGGA	147		

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Qy 606 CGCGGGCGGAGAGCGAGCGCGGCGCTGTGCGCCTTCTTACTAGTCCGCGGATG 665
Db 146 CGCGGGCGGAGAGCGAGCGCGGCGCTGTGCGCCTTCTTACTAGTCCGCGGATG 87
Qy 666 GGTAGAGGAGCGCGCGGCGGAGCGGAGGAGCTTGGCGGCGCTCGGCGGCGCTCCC 725
Db 86 GGTAGAGGAGCGCGCGGCGGAGCGGAGGAGGAGCTTGGCGGCGCTCGGCGGCGCTCCC 27
Qy 726 CCAGCCCTGTCTCTCTCCCTCTTCC 751
Db 26 CCAGCCCTGTCTCTCTCCCTCTTCC 1

RESULT 3
CD389775/c
LOCUS      883 bp      mRNA      linear      EST 30-MAY-2003
DEFINITION AGNCOURT_14305360 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CD389775
VERSION     CD389775.1 GI:31228693
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 883)
            NIH-MGC http://mgc.nci.nih.gov/.
            National Institutes of Health, Mammalian Gene Collection (MGC)
            Unpublished (1999)
            Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jamie Thompson, University of WI
            cDNA Library Preparation: Gina Zastrow-Hayes
            DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
            Clone distribution: Agencourt Bioscience Corporation
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: NDKM72 row: e column: 19
            High quality sequence start: 8
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            Location/Qualifiers
                1..883
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                /db_xref="taxon:9606"
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                cells"
                /lab_host="DH10B Tona"
                /clone_lib="NIH MGC 173"
                /note="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
                LIBR PRIMING - oligo dt; METHOD - full-length enriched;
                LIBR PROVIDER - Bradfield"

FEATURES             source
    source

ORIGIN
Query Match      57.3%; Score 687; DB 6: Length 883;
Best Local Similarity 100.0%; Pred. No. 4.3e-157;
Matches 687; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAACATAAAAGAACCTTTATTTATGAGGCAAGGGATCAACAATACAAAATCAA 60
Db 705 GGAACATAAAAGAACCTTTATTTATGAGGCAAGGGATCAACAATACAAAATCAA 646
Qy 61 AAGCTATCTGGTATTTAACTTTCTTTCTCTGCTGTGTCATGAGAGTTAGATTTATT 120
Db 645 AAGCTATCTGGTATTTAACTTTCTTTCTCTGCTGTGTCATGAGAGTTAGATTTATT 586
Qy 121 TTTACATTTGCTAGTGCCTGATCTGCTCATGAATCTTCTATGCGGAGCTGTGG 180
Db 585 TTTACATTTGCTAGTGCCTGATCTGCTCATGAATCTTCTATGCGGAGCTGTGG 526

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Qy 181 GCAGATTCTTAAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 240
Db 525 GCAGATTCTTAAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 466
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Db 465 TCTGCTTACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 406
Qy 301 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 405 GTGAGGCGCGCAATTAGGAAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 346
Qy 361 TCCAGGTCCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 420
Db 345 TCCAGGTCCTTCAATATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 286
Qy 421 GGGAACTCTCTTTTCCATGAGTACTCTCAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 480
Db 285 GGGAACTCTCTTTTCCATGAGTACTCTCAGTCTCTTCTTCTTCTTCTTCTTCTTCTTCT 226
Qy 481 GCGAATTTGTAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAAT 540
Db 225 GCGAATTTGTAAATGTAAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCAAT 166
Qy 541 TTGCTGTGTGTCGTTGAAGCCTTTGGCCAGCGCGCGGACGCTGGCGGAGCTGGCGGAG 600
Db 165 TTGCTGTGTGTCGTTGAAGCCTTTGGCCAGCGCGCGGACGCTGGCGGAGCTGGCGGAG 106
Qy 601 CTGAGCGCGGGCGGAGAGCGGCGGAGCGCGGCGGCGGAGCTGGCGGAGCTGGCGGAG 660
Db 105 CTGAGCGCGGGCGGAGAGCGGCGGAGCGCGGCGGCGGAGCTGGCGGAGCTGGCGGAG 46
Qy 661 GGGTGGGTAGAGGAGGCGCGCGGCGGAG 687
Db 45 GGGTGGGTAGAGGAGGCGCGCGGCGGAG 19

RESULT 4
BM785208/c
LOCUS      679 bp      mRNA      linear      EST 05-MAR-2002
DEFINITION K-EST0063546 S13KMS581 Homo sapiens cDNA clone S13KMS581-2-G09 5',
            mRNA sequence.
ACCESSION  BM785208
VERSION     BM785208.1 GI:19133440
KEYWORDS   EST.
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE  1 (bases 1 to 679)
            Oh, K.J., Hahn, Y., Oh, J.H., Lee, J.Y., Ahn, H.Y., Chu, M.Y., Kim, M.R.,
            Kim, N.S., Kim, N.S., Sohn, H.Y., Kim, J.M., Park, H.S., Kim, S. and
            Kim, Y.S., Cheong, J.E., Sohn, H.Y., Park, H.S., Kim, S. and
            Kim, Y.S., 2001
            21C Frontier Korean EST Project 2001
            Unpublished (2002)
            Contact: Kim YS
            Genome Research Center
            Korea Research Institute of Bioscience & Biotechnology
            52 Boeun-dong Yuseong-gu, Daejeon 305-333, South Korea
            Tel: +82-42-860-4470
            Fax: +82-42-860-4409
            Email: yongsung@mail.kribb.re.kr
            Plate: 2 row: G column: 09
            High quality sequence stop: 679.
            Location/Qualifiers
                1..679
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                /tissue_type="myeloma"
                /cell_line="KMS-5"

FEATURES             source
    source

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Qy 241 TCTGCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATG 300
 Db 426 TCTGCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATG 367
 Qy 301 GTGAGGCCCGCAATTTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
 Db 366 GTGAGGCCCGCAATTTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 307
 Qy 361 TCCAGGCTCTTCCATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAATCCA 420
 Db 306 TCCAGGCTCTTCCATTTTGTCCACAGCCAGAGGGTCTTTTGAATTTCCAAAATCCA 247
 Qy 421 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAAGTCCCTTTATCCCCA 480
 Db 246 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGTAAAGTCCCTTTATCCCCA 187
 Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTCTCCATTTGAGATGGCATT 540
 Db 186 GCGAATTTGTGAATGTAAACATCATGTTTCCATGGCGTCTCCATTTGAGATGGCATT 127
 Qy 541 TTGCTGTGCTCGTTGAAGCCTTTGGCCGAGCGCGGGAGCGCTGGCGAGCTGGCGGAG 600
 Db 126 TTGCTGTGCTCGTTGAAGCCTTTGGCCGAGCGCGGGAGCGCTGGCGAGCTGGCGGAG 67
 Qy 601 CTGACGCGGGCGGAGAGCGGAGCGCGGGCTGTGGCGCTTCTTGTAGTACGTGGCG 660
 Db 66 CTGACGCGGGCGGAGAGCGGAGCGCGGGCTGTGGCGCTTCTTGTAGTACGTGGCG 7
 Qy 661 GGGTGG 666
 Db 6 GGGTGG 1

RESULT 6
 BG774775/c
 LOCUS 602662641F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4811026 5',
 DEFINITION mRNA sequence.

ACCESSION BG774775
 VERSION BG774775.1 GI:14045092
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NIH-MGC <http://mgc.nci.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-r@mail.nih.gov
 Tissue Procurement: ATCC

cDNA Library Preparation: Ling Hong/Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LUCM1668 row: a column: 11
 High quality sequence stop: 666.
 Location/Qualifiers

FEATURES

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 /db_xref="taxon:9606"
 /clone="IMAGE:4811026"
 /tissue type="Choriocarcinoma"
 /lab host="DH10B (phage-resistant)"
 /clone lib="NIH MGC 21"
 /note="Organ: placenta; Vector: pOTB7; site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Size-selected >500bp

for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN

Query Match 55.3%; Score 663; DB 4; Length 671;
 Best Local Similarity 99.3%; Pred. No. 3.le-151;
 Matches 666; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 Qy 250 TTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATGCGAGGCC 309
 Db 671 TTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATGCGAGGCC 612
 Qy 310 GCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGTCAGGTCC 369
 Db 611 GCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGTCAGGTCC 552
 Qy 370 TTCAATATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCCAGGAACTCC 429
 Db 551 TTCAATATTTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCGAAAATCCAGGAACTCC 492
 Qy 430 TTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAGTAGCCTTTATCCCGAGCAATTTG 489
 Db 491 TTTTCCATGAGTACTCTCAGGTCTCTCTTTGTTAAGTAGCCTTTATCCCGAGCAATTTG 432
 Qy 490 TGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGGCATTTTGGTGTGG 549
 Db 431 TGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGGCATTTTGGTGTGG 372
 Qy 550 TCCGTTGAAGCCTTTGGCCGAGCGCGGAGAGCTTGGCGGAGCTGGGCGAGCTGGACGCG 609
 Db 371 TCCGTTGAAGCCTTTGGCCGAGCGCGGAGAGCTTGGCGGAGCTGGGCGAGCTGGACGCG 312
 Qy 610 GGGCGAGAGCGGAGCGCGGAGAGAGCTTGGCGGAGCTTGGCGGAGCTGGGCGAGCTGGGTA 669
 Db 311 GGGCGAGAGCGGAGCGCGGAGAGAGCTTGGCGGAGCTTGGCGGAGCTGGGCGAGCTGGGTA 252
 Qy 670 GAGGAGCGCGCGGAGCGGAGAGAGCTTGGCGGAGCTTGGCGGAGCTGGGCGAGCTGGGTA 729
 Db 251 GAGGAGCGCGGTGCGGAGCGGAGAGAGCTTGGCGGAGCTTGGCGGAGCTGGGCGAG 192
 Qy 730 CCCTGTCTCTCCCTCTCTTCTGTCCTCCGACTCCCTCCGAGCTCCCGGCGCGCGCCACG 789
 Db 191 CCCTGTCTCTCCCTCTCTTCTGTCCTCCGACTCCCTCCGAGCTCCCGGCGCGCGCCACG 132
 Qy 790 CCCTGCCCTCGCTCCCGAGCGCTCGAGAGGCTTGGCGGAGCTTGGCGGAGCTGGGCGAGCTGG 849
 Db 131 CCCTGCCCTCGCTCCCGAGCGCTCGAGAGGCTTGGCGGAGCTTGGCGGAGCTGGGCGAG 72
 Qy 850 TTGTAAACTTCTCTTCACTAGTAAAGAGCTTCTGCTCTCGAATATTTTCAAGGGCATCCCCACC 909
 Db 71 TTGTAAACTTCTCTTCACTAGTAAAGAGCTTCTGCTCTCGAATATTTTCAAGGGCATCCCCACC 12
 Qy 910 CTGAGCCTGCC 920
 Db 11 GTGAGCCTGCC 1

RESULT 7

BE729901/c

LOCUS

DEFINITION

601564949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925932 5',

mRNA sequence.

ACCSSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Homo sapiens

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

BE729901 912 bp mRNA linear EST 15-SEP-2000
 601564949F1 NIH_MGC_20 Homo sapiens cDNA clone IMAGE:3925932 5',
 mRNA sequence.

BE729901.1 GI:10143893

EST.

Homo sapiens (human)

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 912)

AUTHORS

NIH-MGC <http://mgc.nci.nih.gov/>.

Db 477 GCAGATTCTTAAGCGACCTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCATT 418

Qy 241 TCTGCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATG 300

Db 417 TCTGCTACTTCTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATGCAATG 358

Qy 301 GTGAGCCCGCAATTAGGGAAGAAGCTCTGGAGCCCACTTTGCCATCTACACTGG 360

Db 357 GTGAGCCCGCAATTAGGGAAGAAGCTCTGGAGCCCACTTTGCCATCTACACTGG 298

Qy 361 TCCAGGTCCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 420

Db 297 TCCAGGTCCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 238

Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTGGTCTTTATCCCA 480

Db 237 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTGGTCTTTATCCCA 178

Qy 481 GCGAATTTGTGAATGTAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCAAT 540

Db 177 GCGAATTTGTGAATGTAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCAAT 118

Qy 541 TTGTTGTGTCCTTGAAGCCTTGGCCGAGCGCGGAGCTGGGAGCTGGGCGAG 600

Db 117 TTGTTGTGTCCTTGAAGCCTTGGCCGAGCGCGGAGCTGGGAGCTGGGCGAG 58

Qy 601 CTGACGCGGCGGAGAGCGAGCGCGGCGGCTGTGCGCTTCTTTAGTACGTGC 657

Db 57 CTGACGCGGCGGAGAGCGAGCGCGGCGGCTGTGCGCTTCTTTAGTACGTGC 1

RESULT 9

BX362846/c

LOCUS

DEFINITION BX362846 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
CDNA clone CS0DK004YH20 5-PRIME, mRNA sequence.

ACCESSION

BX362846

VERSION

BX362846.2 GI:46552294

KEYWORDS

EST.

SOURCE

Homo sapiens

ORGANISM

Homo sapiens (human)

REFERENCE

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

Li, W.B., Gruber, C., Jessee, J. and Polayes, D.

Full-length cDNA libraries and normalization

Unpublished (2001)

On May 5, 2003 this sequence version replaced gi:30390679.

Contact: Genoscope

Genoscope - Centre National de Sequenage

2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime

end enriched, double-strand cDNA was digested with NotI and cloned

into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library

was normalized. Library was constructed by Life Technologies, a

division of Invitrogen. This sequence belongs to sequence cluster

980.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?c=CS0DK004YH20&f=980.r.

Location/Qualifiers

1. .660

/organism="Homo sapiens"

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/db_xref="taxon:9606"

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/cell_line="HELA"

/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"

/note="1st strand cDNA was primed with a NotI-oligo(dT)

primer. Five prime end enriched, double-strand cDNA was

digested with NotI and EcoRV sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

sites of the pCMVSPORT 6 vector. Library was normalized."

FEATURES

source

ORIGIN

Query Match 54.8%; Score 657; DB 5; Length 660;

Best Local Similarity 100.0%; Pred.No. 9e-150;

Matches 657; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGAACCTAAAAAGAACCTTTATTTAGGGCAAGGGGATGCAAAACAATACAAAATCAA 60

Db 657 GGAACCTAAAAAGAACCTTTATTTAGGGCAAGGGGATGCAAAACAATACAAAATCAA 598

Qy 61 AAGCTTAATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAAATGAGAGTATGATTTTATT 120

Db 597 AAGCTTAATCTGGTATTTAACTTTCTTCTCTGCTTGTCAAAATGAGAGTATGATTTTATT 538

Qy 121 TTTACATTTGCTAAGTGTCTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180

Db 537 TTTACATTTGCTAAGTGTCTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 478

Qy 181 GCAGATTTCCTTAAGCGACCTTTTGGGACAACTTTATCAGGAGGAGGGAATCTGCTCATT 240

Db 477 GCAGATTTCCTTAAGCGACCTTTTGGGACAACTTTATCAGGAGGAGGGAATCTGCTCATT 418

Qy 241 TCTGCTTACTTCTTTTCCCTTCTGCTTCTATGTTACTACAAAATAGTCAATGCAATGCAATG 300

Db 417 TCTGCTTACTTCTTTTCCCTTCTGCTTCTATGTTACTACAAAATAGTCAATGCAATGCAATG 358

Qy 301 GTGAGGCCCGCAATTAGGGAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360

Db 357 GTGAGGCCCGCAATTAGGGAAGAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 298

Qy 361 TCCAGGTCCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 420

Db 297 TCCAGGTCCTTCAATTAATTTGTCCACAGCCAGAGGGTCTTTTGAATTTTCAAAAATCCA 238

Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTGGTCTTTATCCCA 480

Db 237 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCCTCTTGTAAAGTGGTCTTTATCCCA 178

Qy 481 GCGAATTTGTGAATGTAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCAAT 540

Db 177 GCGAATTTGTGAATGTAACATCATGTTTCCATGGCGTGTCCATTTGAGATGGCAAT 118

Qy 541 TTGTTGTGTCCTTGAAGCCTTGGCCGAGCGCGGAGCTGGGAGCTGGGCGAG 600

Db 117 TTGTTGTGTCCTTGAAGCCTTGGCCGAGCGCGGAGCTGGGAGCTGGGCGAG 58

Qy 601 CTGACGCGGCGGAGAGCGAGCGCGGCGGCTGTGCGCTTCTTTAGTACGTGC 657

Db 57 CTGACGCGGCGGAGAGCGAGCGCGGCGGCTGTGCGCTTCTTTAGTACGTGC 1

RESULT 10

CD177393/c

LOCUS

CD177393

DEFINITION

AGENCOURT_13977124 NIH_MGC_173 Homo sapiens cDNA 5', mRNA sequence.

ACCESSION

CD177393

VERSION

CD177393.1 GI:30863968

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

1 (bases 1 to 705)

NTH-MGC http://mgs.nci.nih.gov/

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs@mail.nih.gov

Tissue Procurement: Dr. Jamie Thompson, University of WI

cDNA Library Preparation: Gina Zastrow-Haves

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov
 Plate: NDKM38 row: c column: 22
 High quality sequence start: 17
 High quality sequence stop: 670.
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 /tissue_type="embryonic trophoblasts, made from WA01 stem cells"
 /lab_host="DH10B Tona"
 /clone_lib="NIH_MGC 173"
 /notes="Vector: pDONR201; Site 1: attP2; Site 2: attP1;
 LIBR_PRIMING - oligo dt; METHOD - full-length enriched;
 LIBR_PROVIDER - Bradfield"

FEATURES

source

ORIGIN

Query Match 54.4%; Score 652.8; DB 6; Length 705;
 Best Local Similarity 98.9%; Pred. No. 9.7e-149;
 Matches 657; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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 Qy 61 AAGCTTATCTGGTATTAACTTTCTTCCTGCTGCTCAATGAGAGTTAGATTTATT 120
 Db 624 AAGCTTATCTGGTATTAACTTTCTTCCTGCTGCTCAATGAGAGTTAGATTTATT 565
 Qy 121 TTTACATTTGCTAGTGTCTGATCTCTCATGAATCCCTTCTATGGGGAAGCTGTGGG 180
 Db 564 TTTACATTTGCTAGTGTCTGATCTGCTCCCATGAAATCCCTTCTATGGGGAAGCTGTGGG 505
 Qy 181 GCAGATTCTTAAGCGACCCCTTTGGGCAACTCTTATCGAGGAGGAGCGAACTGCTCAT 240
 Db 504 GCAGATTCTTAAGCGACCCCTTTGGGCAACTCTTATCGAGGAGGAGCGAACTGCTCAT 445
 Qy 241 TCTGCCCTACTCTTCTCCCTCTGCTTCATGTGACTACAAATAGTCAATGCAATGCAATG 300
 Db 444 TCTGCCCTACTCTTCTCCCTCTGCTTCATGTGACTACAAATAGTCAATGCAATGCAATG 385
 Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
 Db 384 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 325
 Qy 361 TCCAGGTCCTTCATTTATTTTGTCCACAGCAGAGGGCTTTTGTGATTTTCCAAATATCCA 420
 Db 324 TCCAGGTCCTTCATTTATTTTGTCCACAGCAGAGGGCTTTTGTGATTTTCCAAATATCCA 265
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 Db 264 GGGAACTCTTTCCATGAGTACTCTCAGGTCCTCTTGTGATGAGTACCTTTATCCCA 205
 Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCATT 540
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 Qy 541 TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGCGGACGCTGGCGAGCTGGCGAG 600
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 Qy 601 CTGACCGCGGCGGAGCGGAGCGCGCGGCTGTGCGGCTTCTTAGTACGTGCGGC 660
 Db 84 CTGACCGCGGCGGAGCGGAGCGCGCGGCTGTGCGGCTTCTTAGTACGTGCGGC 25
 Qy 661 GGGT 664
 Db 24 GGTT 21

, RESULT 11

BQ646470/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BQ646470 670 bp mRNA linear EST 15-JUL-2002
 AGENCOURT_8286408 NIH_MGC_100 Homo sapiens cDNA clone IMAGE:6299585
 5', mRNA sequence.
 BQ646470
 BQ646470.1 GI:21770642
 EST.
 Homo sapiens (human)
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: CGAP (Stanford)
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCM2512 row: h column: 18
 High quality sequence stop: 640.
 Location/Qualifiers
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 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6299585"
 /tissue_type="hepatocellular carcinoma, cell line"
 /lab_host="DH10B (phage-resistant)"
 /clone_lib="NIH_MGC_100"
 /notes="Organ: liver; Vector: pOTB7; Site 1: XhoI; Site 2:
 EcoRI; cDNA made by oligo-dT priming. Directionally cloned
 into EcoRI/XhoI sites using the following 5' adaptor:
 GGCACGAG(G). Size-selected >500bp for average insert size
 1.8kb. Library constructed by Ling Hong in the laboratory
 of Gerald M. Rubin (University of California, Berkeley)
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript
 II RT (Life Technologies). Note: this is a NIH_MGC
 Library."

FEATURES

source

ORIGIN

Query Match 54.4%; Score 652; DB 5; Length 670;
 Best Local Similarity 100.0%; Pred. No. 1.5e-148;
 Matches 652; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GGAACATAAAGAACTTTATTTATTGAGGCAAGGGATGCAAAACAATACAAATCAA 60
 Db 652 GGAACATAAAGAACTTTATTTATTGAGGCAAGGGATGCAAAACAATACAAATCAA 593
 Qy 61 AAGCTTATCTGGTATTAACTTTCTCTCTCTGCTCAAAATGAGAGTTAGATTTATT 120
 Db 592 AAGCTTATCTGGTATTAACTTTCTCTCTCTGCTCAAAATGAGAGTTAGATTTATT 533
 Qy 121 TTTACATTTGCTAGTGTCTGATCTGCTCATGAATCCCTTCTATGGGGAAGCTGTGGG 180
 Db 532 TTTACATTTGCTAGTGTCTGATCTGCTCATGAATCCCTTCTATGGGGAAGCTGTGGG 473
 Qy 181 GCAGATTCTTTAAGCGACCCCTTTGGGACAACTCTTATCGAGGAGGAGCGAACTGCTCAT 240
 Db 472 GCAGATTCTTTAAGCGACCCCTTTGGGACAACTCTTATCGAGGAGGAGCGAACTGCTCAT 413
 Qy 241 TCTGCCCTACTCTTCTCCCTCTGCTTCATGTGACTACAAATAGTCAATGCAATG 300
 Db 412 TCTGCCCTACTCTTCTCCCTCTGCTTCATGTGACTACAAATAGTCAATGCAATG 353
 Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
 Db 352 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 293

Qy	361	TC	CAGGTCCTT	CATTATTT	GTGCACAGC	CAGAGGTC	TTTTCATTTT	CCAAAAATCCA	420
Db	292	TCC	AGGTCCTT	CATTATTT	GTGCACAGC	CAGAGGTC	TTTTCATTTT	CCAAAAATCCA	233
Qy	421	GGG	AACCTCTT	TTCCATGAGT	ACTCTCAGGTC	CCTCCTTTGTTAAGTAGC	CTTTATCCCCA	480	
Db	232	GGG	AACCTCTT	TTCCATGAGT	ACTCTCAGGTC	CCTCCTTTGTTAAGTAGC	CTTTATCCCCA	173	
Qy	481	GC	GAATTTG	TGAATGTAAACAT	CATATGGTTTCCATGGCGTC	TCCATTTGAGATGGCATT	540		
Db	172	GCG	AATTTG	TGAATGTAAACAT	CATATGGTTTCCATGGCGTC	TCCATTTGAGATGGCATT	113		
Qy	541	TT	GTGTGTC	CGTTGAAGCCTT	GGCGAGCGCGGCGAGCGCTGTGGCGAGCTGGGCGAG	600			
Db	112	TT	GTGTGTC	CCGTTGAAGCCTT	GGCGAGCGCGGCGAGCGCTGTGGCGAGCTGGGCGAG	53			
Qy	601	CT	GACCGGGCGG	GAGAGGCGAGCG	CGGGCGGCTGTGCGCTTCCCTTAGTA	652			
Db	52	CT	GACCGGGCGG	GAGAGGCGAGCG	CGGGCGGCTGTGCGCTTCCCTTAGTA	1			

RESULT 12	737 bp	linear	EST 27-FEB-2001
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LOCUS	602437371F1	NIH_MGC_46 Homo sapiens cDNA clone IMAGE:4555216 5',	
DEFINITION	mRNA sequence.		
ACCESSION	BG339527		
VERSION	BG339527.1	GI:13145965	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
	1 (bases 1 to 737)		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/ .		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: ATCC		
	cDNA Library Preparation: Ling Hong/Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Incyte Genomics, Inc.		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: L12CM1255	row: n	column: 17
	High quality sequence stop: 724.		

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RESULT 13	REFERENCE
BM541317/c	AUTHORS
LOCUS	TITLE
DEFINITION	JOURNAL
	COMMENT
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	

ORIGIN

Query Match 54.3%; Score 651.6; DB 4; Length 737;
Best Local Similarity 96.9%; Pred. NO. 1.9e-148;
Matches 695; Conservative 0; Mismatches 17; Indels 5; Gaps 3;

Qy		9	AAAGAACCTTTATTTATTGAGGCAAGGGGATCCAAAACATACAAAAATCAAAGCTTAT	68
Db		712	AAAAAGACTTTTAGTTATGAGGCCAAGGGGATGCNAACA--TACAAATCAAAGCTCAT	655
Qy		69	CTGGTATTTAACTTTCTTCCTCTGCTGTGTCAAAATGAGAGTTAGATTTTATTTTTACATT	128
Db		654	CTGGTATTTAACTTTCTTCCTCTGCTGTGTCAAAATGAGAGTTAGATTTTATTTTTACATT	595
Qy		129	TGCTAAGTGTCCTGATCTGCTCATGAATACTCTTCTATGSGGGAAGCTGTGGGCGAGATTC	188
Db		594	TGCTAAGTGTCCTGATCTGCTCATGAATACTCTTCTATGSGGGA--CTGTGGGCGAGATTC	537
Qy		189	CTTAAGCGACCCTTTGGGACAACTCTTATCAGGCGAGGAGGAACCTGCTCATTTCTGCCTA	248
Db		536	CTTAAGCGACCCTTTGGGACAACTCTTATCAGGCGAGGAGGAACCTGCTCATTTCTGCCTA	477
Qy		249	CTTCTTTTCCCCTCTGCTTCAATGTGTACTACAAAATAGTCAATTCGATGCAAATGCTGAGGCC	308
Db		476	CTTCTTTTCCCCTCTGCTTCAATGTGTACTACAAAATAGTCAATTCGATGCAAATGCTGAGGCC	417
Qy		309	CGCAATTAGGGAAGAAGAGCTCTGGAGGCCACTTTGGCCATCTACACTGGTCCAGGTC	368
Db		416	CGCAATTAGGGAAGAAGAGCTCTGGAGGCCACTTTGGCCATCTACACTGGTCCAGGTC	357
Qy		369	CTTCAATTATTTGTCCAAGCCAGAGGGTCTTTTGATTTTCCAAAATCCAGGGAACCTC	428
Db		356	CTTCAATTATTTGTCCAAGCCAGAGGGTCTTTTGATTTTCC--AAAAATCCAGGGAACCTC	298
Qy		429	CTTTTCCATGAGTACTCTCAGGTCCTCTTTGTTAGTAGGCTTTATCCCCAGGAAATTT	488
Db		297	CTTTTCCATGAGTACTCTCAGGTCCTCTTTGTTAGTAGGCTTTATCCCCAGGAAATTT	238
Qy		489	GTCAAAATGTAAACATCATGTGTTTCCATGGCGTGTCCATTTGAGATGGCAATTTGTGTGTG	548
Db		237	GTCAAAATGTAAACATCATGTGTTTCCATGGCGTGTCCATTTGAGATGGCAATTTGTGTGTG	178
Qy		549	GTCGGTTGAAGCCTTGGCCGAGCGCGGCGGAGCGCTGGGCGAGCTGGGCGAGCTGAGCGC	608
Db		177	GTCGGTTGAAGCCTTGGCCGAGCGCGGCGGAGCGCTGGGCGAGCTGGGCGAGCTGAGCGC	118
Qy		609	GGGCGGAGAGGCGAGCGCGGGGGTGTGTGCGCTTCTTTAGTACGTGCGGCGGGTGGGT	668
Db		117	GGGCGGAGAGGCGAGCGCGGGGGTGTGTGCGCTTCTTTAGTACGTGCGGCGGGTGGGT	58
Qy		669	AGAGGAGGCGCGCGGAGCGGAGAGCCTTGGCGGGCGCTCGGAGGCGCTGCC	725
Db		57	AGAGGAGGCGCGCGGAGCGGAGAGCCTTGGCGGGCGCTCGGAGGCGCTGCC	1

BMS541317//	LOCUS	DEFINITION	ACCESSION	REFERENCE
			VERSION	AUTHORS
			KEYWORDS	TITLE
			SOURCE	JOURNAL
		ORGANISM		COMMENT

FEATURES	source	http://image.llnl.gov	
		Plate: LLAM2186 row: p column: 07	
KEYWORDS	SOURCE	High quality sequence stop: 657.	
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		/db_xref="taxon:9606"	
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		/tissue_type="leiomyosarcoma"	
COMMENT	COMMENT	/lab_host="DH10B (phage-resistant)"	
		/clone_lib="NIH_MGC_71"	
ORIGIN	source	/note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;	
		Site 2: SalI; Cloned unidirectionally. Primer: Oligo dt.	
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FEATURES	source	/mol_type="mRNA"	
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		/tissue_type="mixed (pool of 40 RNAs)"	
ORIGIN	source	/lab_host="DH10B (TI-phage-resistant)"	
		/clone_lib="NIH_MGC_142"	
ORIGIN	source	/note="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);	
		Site 2: SfiI (ggccgcctcgcc); Double-stranded cDNA was	
ORIGIN	source	prepared from a pool of 40 cell line polyA+ RNAs (bladder	
		- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -	
ORIGIN	source	4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,	
		kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell - 5.2%,	
ORIGIN	source	ovary - 4%, pharynx - 2.5%, prostate - 4.3%, salivary	
		gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were	
ORIGIN	source	used in cloning as follows:	
		5'-AACGAGTGGTATCAACGACGAGTGCCATTACGCGCGG-3' and	
ORIGIN	source	5'-ATTCTAGAGCGCGGCGCGACATG-dt(30)NN-3'. Full-length	
		enriched library was constructed using the Clontech	
ORIGIN	source	Creator SMART kit and size-selected to contain the >0.5 kb	
		size fraction (other fractions present in NIH_MGC_141).	
ORIGIN	source	Library created in the laboratory of M. Brownstein (NIH,	
		NIH). Note: this is a NIH_MGC Library."	
ORIGIN	source	Query Match 53.9%; Score 646.6; DB 5; Length 843;	
		Best Local Similarity 99.4%; Pred. No. 3.3e-147;	
ORIGIN	source	Matches 649; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
ORIGIN	source	Qy 1 GGAACATAAAAGAACCTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAA 60	
		Db 648 GGAACATAAAAGAACCTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAA 589	
ORIGIN	source	Qy 61 AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120	
		Db 588 AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 529	
ORIGIN	source	Qy 121 TTTACATTTGTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGCGGGAAGCTGTGG 180	
		Db 528 TTTACATTTGTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGCGGGAAGCTGTGG 469	
ORIGIN	source	Qy 181 GCAGATTCCTTAAGCGACCTTTGGGACAACTCTTATCAGGAGGAGGCACTGCTCAT 240	
		Db 468 GCAGATTCCTTAAGCGACCTTTGGGACAACTCTTATCAGGAGGAGGCACTGCTCAT 409	
ORIGIN	source	Qy 241 TCTGCCTACTTCTTCCCTCTCTGCTTCATGTGTACTACAAATAGTCATTCATGCAATG 300	
		Db 408 TCTGCCTACTTCTTCCCTCTCTGCTTCATGTGTACTACAAATAGTCATTCATGCAATG 349	
ORIGIN	source	Qy 301 GTGAGGCGCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACATGG 360	
		Db 348 GTGAGGCGCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACATGG 289	
ORIGIN	source	Qy 361 TCCAGGTCTCTCATATTATTTGTCACAGCCAGAGGCTTTTTCATTTCCAAATCCA 420	
		Db 288 TCCAGGTCTCTCATATTATTTGTCACAGCCAGAGGCTTTTTCATTTCCAAATCCA 229	
ORIGIN	source	Qy 421 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTTGTGTAAGTAGCCCTTTATCCCA 480	
		Db 228 GGGAACTCCTTTTCCATGAGTACTCTCAGGTCTCTTGTGTAAGTAGCCCTTTATCCCA 169	
ORIGIN	source	Qy 481 GCGAATTTGTGAATGAAACATCATGTTTCCATGCGGTGTCCATTGAGATGGCAATT 540	
		Db 168 GCGAATTTGTGAATGAAACATCATGTTTCCATGCGGTGTCCATTGAGATGGCAATT 109	
ORIGIN	source	Qy 541 TTGTTGTGTCCTTGAAGCCCTTGGCGAGCGCGGAGCGCTGGCGGAGCTGGCGGAG 600	
		Db 108 TTGTTGTGTCCTTGAAGCCCTTGGCGAGCGCGGAGCGCTGGCGGAGCTGGCGGAG 49	
ORIGIN	source	Qy 601 CTGACGCGGCGGAGAGGCGGAGCGGCGGCTGTGCGGCTTCCCTT 648	
		Db 48 CTGACGCGGCGGAGAGGCGGAGCGGCGGCTGTGCGGCTTCCCTT 1	
ORIGIN	source	Query Match 53.9%; Score 646.6; DB 5; Length 843;	
		Best Local Similarity 99.4%; Pred. No. 3.3e-147;	
ORIGIN	source	Matches 649; Conservative 0; Mismatches 4; Indels 0; Gaps 0;	
ORIGIN	source	Qy 1 GGAACATAAAAGAACCTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAA 60	
		Db 655 GGAACATAAAAGAACCTTTATTATTGAGGCAAGGGGATGCAACATACAAATCAA 596	
ORIGIN	source	Qy 61 AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 120	
		Db 595 AAGCTTATCTGGTATTAACTTTCTCTGCTTGTCAAATGAGAGTTAGATTTTATT 536	
ORIGIN	source	Qy 121 TTTACATTTGTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGCGGGAAGCTGTGG 180	
		Db 535 TTTACATTTGTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGCGGGAAGCTGTGG 476	
ORIGIN	source	Qy 181 GCAGATTCCTTAAGCGACCTTTGGGACAACTCTTATCAGGAGGAGGCACTGCTCAT 240	
		Db 475 GCAGATTCCTTAAGCGACCTTTGGGACAACTCTTATCAGGAGGAGGCACTGCTCAT 416	
ORIGIN	source	Qy 241 TCTGCCTACTTCTTCCCTCTCTGCTTCATGTGTACTACAAATAGTCATTCATGCAATG 300	
		Db 415 TCTGCCTACTTCTTCCCTCTCTGCTTCATGTGTACTACAAATAGTCATTCATGCAATG 356	
ORIGIN	source	Qy 301 GTGAGGCGCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACATGG 360	
		Db 301 GTGAGGCGCGCAATTAGGAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACATGG 360	

RESULT 14
BU594774/c
LOCUS
DEFINITION AGNCOURT_8843010 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6450402
5', mRNA sequence.
ACCESSION BU594774
VERSION BU594774.1 GI:23246533


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into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 53.9%; Score 646.4; DB 5; Length 940;
Best Local Similarity 99.8%; Pred. No. 3.7e-147;
Matches 647; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Qy |
61 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTCAAAATCAGAGTTAGATTTTATT 120
Db |
588 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTCAAAATCAGAGTTAGATTTTATT 529
Qy |
121 TTTCATTTGCTAAGTCTGCTGATCTGCTCATGAAATCCCTTATGCGGGAAGCTGTGGG 180
Db |
528 TTTCATTTGCTAAGTCTGCTGATCTGCTCATGAAATCCCTTATGCGGGAAGCTGTGGG 469
Qy |
181 GCAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAAGTCTCAT 240
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Qy |
241 TCTGCCTACTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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Db |
288 TCCAGTCTCTTCAATATTTTGTCCACAGCGAGGCTCTTTTGAATTTTCCAAAATCCA 229
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421 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 480
Db |
228 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 169
Qy |
481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 540
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168 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 109
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541 TTGGTGTGTCCTGTTGAAGCTTTGGCGAGCGCGCGGACGCTGTGGCGAGCTGTGGCGAG 600
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108 TTGGTGTGTCCTGTTGAAGCTTTGGCGAGCGCGCGGACGCTGTGGCGAGCTGTGGCGAG 49
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Db |
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RESULT 17
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LOCUS 602430639f1 NIH_MGC_18 Homo sapiens cDNA clone IMAGE:4548656 5',
DEFINITION mRNA sequence.
, ACCESSION BG332809

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VERSION BG332809.1 GI:13139247
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 681)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabs-remail.nih.gov
Tissue Procurement: DCTD/DTp/Gazdar
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCML238 row: m column: 09
High quality sequence stop: 660.
FEATURES
Location/Qualifiers
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/notes="Organ: lung; Vector: pOTB7; Site 1: XhoI; Site 2:
into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGCAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

ORIGIN
Query Match 53.8%; Score 645; DB 4; Length 681;
Best Local Similarity 99.8%; Pred. No. 7.8e-147;
Matches 656; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

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Db |
656 GGAACTAAAAAGAACTTTATTTGAGGCGAAGGGATGCAAAACAATCAAAATCAA 598
Qy |
61 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db |
597 AAGCTTATCTGGTATTTAACTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 538
Qy |
121 TTTCATTTGCTAAGTCTGCTGATCTGCTCATGAAATCCCTTATGCGGGAAGCTGTGGG 180
Db |
537 TTTCATTTGCTAAGTCTGCTGATCTGCTCATGAAATCCCTTATGCGGGAAGCTGTGGG 478
Qy |
181 GCAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAAGTCTCAT 240
Db |
477 GCAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGAGCGAAGTCTCAT 418
Qy |
241 TCTGCCTACTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300
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417 TCTGCCTACTCTTTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 358
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301 GTGAGGCGCGCAATTAGGGAAGAAAGAACTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
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297 TCCAGTCTCTTCAATATTTTGTCCACAGCGAGGCTCTTTTGAATTTTCCAAAATCCA 238
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Db 237 GGAACCTCCTTTTCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGCCCTTTATCCCA 178
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Qy 541 TTGTTGTGTCCTGTTGAAGCCTTTGGCGAGCGCGGGGAGCGTCTGGCGAGCTGGCGAG 600
Db 117 TTGTTGTGTCCTGTTGAAGCCTTTGGCGAGCGCGGGGAGCGTCTGGCGAGCTGGCGAG 58
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RESULT 18
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LOCUS
DEFINITION BU502376 592 bp mRNA linear EST 12-SEP-2002
5', mRNA sequence.
AGENCOURT_8905908 NIH_MGC_142 Homo sapiens cDNA clone IMAGE:6452219

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ACCESSION BU502376
VERSION BU502376.1 GI:22806955

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KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

```

```

REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

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Tissue Procurement: NCI
cDNA Library Preparation: Michael Brownstein Laboratory
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Clone distribution: Agencourt Bioscience Corporation
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov

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High quality sequence stop: 541.
Location/Qualifiers

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Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was
prepared from a pool of 40 cell line polyA+ RNAs (bladder
- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -
4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,
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gland - 1.3%, and skin - 2.3%). 5' and 3' adaptors were
used in cloning as follows:
5'-AAGCAGTGTATCAACGAGAGTGGCCATACGCGCGG-3' and
5'-ATTCTAGAGCGGAGCGCGGCGGAGATG-dt(30)NN-3'. Full-length
enriched library was constructed using the Clontech
Creator SMART kit and size-selected to contain the >0.5 kb
size fraction (other fractions present in NIH_MGC_141).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."

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FEATURES
source

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size fraction (other fractions present in NIH_MGC_141).
Library created in the laboratory of M. Brownstein (NIMH,
NIH). Note: this is a NIH_MGC Library."

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RESULT 19
BU602356/c
LOCUS
DEFINITION

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AGENCOURT_10014821 NIH_MGC_142 Homo sapiens cDNA clone
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ACCESSION BU602356
VERSION BU602356.1 GI:23254115

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KEYWORDS EST.
SOURCE Homo sapiens (human)

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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

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REFERENCE NIH-MGC http://mgi.nci.nih.gov/.
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.

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Clone distribution: Agencourt Bioscience Corporation
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http://image.llnl.gov

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FEATURES
source

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Site 2: SfiI (ggcgctctggcc); Double-stranded cDNA was
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Qy	208	CAACTCTTATCAGGAGGAGCGAACTGCTCATTTCTGCGCTACTTCTTTCCTTCTGCTTC	267
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KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/		
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)		
TITLE	Unpublished (1999)		
JOURNAL	Contact: Robert Strausberg, Ph.D.		
COMMENT	Email: cgapbs-r@mail.nih.gov		
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	cDNA Library Preparation: Rubin Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
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ORIGIN			
	Query Match	53.2%; Score 638; DB 5; Length 655;	
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Db	578	AAGCTTATCTGTATTTAACCTTTCTCTCTCTGTCTTCAATGAGAGTTAGATTATT	519
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Db	518	TTTACATTTGCTAAGTGTCTGATCTGCTCAATGAATCTTCTATGGGGAAGCTGTGG	459
Qy	181	GCAGATTCTTAAAGCGACCTTTGGGCAACCTTTTATCAGGAGAGCGAACTGCTCAT	240
Db	458	GCAGATTCTTAAAGCGACCTTTGGGCAACCTTTTATCAGGAGAGCGAACTGCTCAT	399
Qy	241	TCGTGCTACTTCTTCCCTTCTGCTTCATGTACTACAAAATAGTCAATGCAATG	300
Db	398	TCGTGCTACTTCTTCCCTTCTGCTTCATGTACTACAAAATAGTCAATGCAATG	339


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Plate: LLAM11407 row: m column: 10
High quality sequence stop: 651.
Location/Qualifiers
1. .657
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5164209"
/tissue_type="medulla"
/lab_host="DH10B"
/clone_lib="NIH_MGC_119"
/note="Organ: brain; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: EcoRV (destroyed); RNA source normal medulla from anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb, insert size range 0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 52.9%; Score 634.4; DB 4; Length 657;
Best Local Similarity 99.8%; Pred. No. 3.1e-144;
Matches 635; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 GGAACATAAAGAACCTTTATTATTCAGGCGAGGGATGCAACCAATACAAATCAA 60
Db |||||||
Qy 636 GGAACATAAAGAACCTTTATTATTCAGGCGAGGGATGCAACCAATACCAATCAA 577
Db |||||||
Qy 61 AAGCTTATCTGGTATTAACTTTTCTTCTCTGCTCAAAATGAGAGTTAGATTTTATT 120
Db |||||||
Qy 576 AAGCTTATCTGGTATTAACTTTTCTTCTCTGCTCAAAATGAGAGTTAGATTTTATT 517
Db |||||||
Qy 121 TTATCATTTGTAAGTCTCGTATCTCTCATGAATCTCTTATGCGGGAAGCTGTGGG 180
Db |||||||
Qy 516 TTATCATTTGTAAGTCTCGTATCTCTCATGAATCTCTTATGCGGGAAGCTGTGGG 457
Db |||||||
Qy 181 GCAGATTCCTTAAGCGACCTTTGGGACACTCTTATCAGGAGGAGCGAAGCTCTCAT 240
Db |||||||
Qy 456 GCAGATTCCTTAAGCGACCTTTGGGACACTCTTATCAGGAGGAGCGAAGCTCTCAT 397
Db |||||||
Qy 241 TCTGCTTACTTCTTCTCTGCTTCTCATGTGTACTACAAAATAGTTCATTCGATGCAATG 300
Db |||||||
Qy 396 TCTGCTTACTTCTTCTCTGCTTCTCATGTGTACTACAAAATAGTTCATTCGATGCAATG 337
Db |||||||
Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db |||||||
Qy 336 GTGAGGCCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 277
Db |||||||
Qy 361 TCCAGGTCCTTCATTTATTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAATCCA 420
Db |||||||
Qy 276 TCCAGGTCCTTCATTTATTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAATCCA 217
Db |||||||
Qy 421 GGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCTCTTTGTAAAGTAGCCCTTTATCCCCA 480
Db |||||||
Qy 216 GGGAACCTCTTTCCATGAGTACTCTCAGGTCCTCTCTTTGTAAAGTAGCCCTTTATCCCCA 157
Db |||||||
Qy 481 GCGAATTTGTGAATGAACAATCATGTTTCCATGGCGGTGTTCCATTTGAGATGGCAATT 540
Db |||||||
Qy 156 GCGAATTTGTGAATGAACAATCATGTTTCCATGGCGGTGTTCCATTTGAGATGGCAATT 97
Db |||||||
Qy 541 TTGCTGTGTCCTGTTGAAGCCTTGGCGAGCGCGGCGAGCGTGGCGAGCTGGGCGAG 600
Db |||||||
Qy 96 TTGCTGTGTCCTGTTGAAGCCTTGGCGAGCGCGGCGAGCGTGGCGAGCTGGGCGAG 37
Db |||||||
Qy 601 CTGACCGCGGCGGAGGCGAGCGCGGCGGCTG 636
Db |||||||
Qy 36 CTGACCGCGGCGGAGGCGAGCGCGGCGGCTG 1
Db |||||||

FEATURES
source
1. 645
/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:3608925"
/tissue_type="endometrium, adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_44"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."
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Db      286 GAGAGCGGAGCGCGGGCTGTGCGCCTTCTTAGTAGCTGCGCGCGGGTGGGTAGAGGG 227
Qy      675 AGCGCGCGCGGAGCGGAGGAGCCTTGGCGGCGCTCGGCGAGCGGCGCTCCCGCCAGCCCTG 734
Db      226 AGCGCGCGCGGAGCGGAGGAGCCTTGGCGGCGCTCGGCGAGCGGCGCTCCCGCCAGCCCTG 167
Qy      735 TCTCTCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 794
Db      166 TCTCTCTCCCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTT 107
Qy      795 CCTCTCGCTCCCGACCCCGCTCGAGAGCGCTCGCGCCGCCAGACAGAGGTTCTTCTGTA 854
Db      106 CCTCTCGCTCCCGACCCCGCTCGAGAGCGCTCGCGCCGCCAGACAGAGGTTCTTCTGTA 47
Qy      855 AACTTCTCTTCTAGTAGAAACGCTCTCTCTCTCGAATATTTTCAGGCG 900
Db      46 AACTTCTCTTCTAGTAGAAACGCTCTCTCTCTCGAATATTTTCAGGCG 1

RESULT 24
BQ050753/c
LOCUS   BQ050753
DEFINITION AGNCOURT_6808933 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5784763
5' mRNA sequence.
ACCESSION BQ050753
VERSION   BQ050753.1 GI:19810093
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 655)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Agencourt Bioscience Corporation
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1AM12870 row: m column: 20
          High quality sequence stop: 654.
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            /db_xref="taxon:9606"
            /clone="IMAGE:5784763"
            /tissue_type="leiomyosarcoma"
            /lab_host="DH10B (phage-resistant)"
            /note="Organ: uterus; Vector: pCMV-SPORT6; Site 1: NotI;
            Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
            Average insert size 2.1 kb."

FEATURES
source
Query Match 52.7%; Score 632; DB 5; Length 655;
Best Local Similarity 100.0%; Pred. No. 1.2e-143;
Matches 632; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGAAGCTAAAGAACTTATTTATTGAGGCGAGGGATCAACATCAAAAAATCAA 60
Db      632 GGAAGCTAAAGAACTTATTTATTGAGGCGAGGGATCAACATCAAAAAATCAA 573
Qy      61 AAGCTTATCTGATTTAACTTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTATT 120
Db      572 AAGCTTATCTGATTTAACTTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTATT 513
Qy      121 TTTACATTTGTAAGTGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG 180
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Db      512 TTTACATTTGTAAGTGTCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAGCTGTGGG 453
Qy      181 GCAGATTCTTAAAGCGAGCCCTTTGGGCAACTCTTTATCAGGAGGAGCGAACTGCTCATT 240
Db      452 GCAGATTCTTAAAGCGAGCCCTTTGGGCAACTCTTTATCAGGAGGAGCGAACTGCTCATT 393
Qy      241 TCTGCTACTTCTTTTCCCTTCTGCTTCATGTGTAATAAAATAGTCAATGCAATG 300
Db      392 TCTGCTACTTCTTTTCCCTTCTGCTTCATGTGTAATAAAATAGTCAATGCAATG 333
Qy      301 GTGAGGCCCGCAATTAGGAAAGAAAGCTCTGAGAGCCCACTTTGCCATCTCTACACTGG 360
Db      332 GTGAGGCCCGCAATTAGGAAAGAAAGCTCTGAGAGCCCACTTTGCCATCTCTACACTGG 273
Qy      361 TCCAGGTCTCTTATTATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTCCAAAAATCCA 420
Db      272 TCCAGGTCTCTTATTATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTCCAAAAATCCA 213
Qy      421 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGAAGTAGCCCTTTATCCCCA 480
Db      212 GGGAACTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTTGAAGTAGCCCTTTATCCCCA 153
Qy      481 GCGAATTTGTAAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 540
Db      152 GCGAATTTGTAAATGTAAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAATT 93
Qy      541 TTGCTGTGTCCTGTTGAAGCTTTGGCGGAGCGCGGCGGCGCTGGCGGAGCTGGCGGCGAG 600
Db      92 TTGCTGTGTCCTGTTGAAGCTTTGGCGGAGCGCGGCGGCGCTGGCGGAGCTGGCGGCGAG 33
Qy      601 CTGACCGCGGGCGGAGAGCGGCGGCGGCGGCGGCGG 632
Db      32 CTGACCGCGGGCGGAGAGCGGCGGCGGCGGCGG 1

RESULT 25
BQ335520/c
LOCUS   BQ335520
DEFINITION 602403994F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4541711 5',
mRNA sequence.
ACCESSION BQ335520
VERSION   BQ335520.1 GI:13141958
KEYWORDS EST.
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 856)
          NIH-MGC http://mgi.nci.nih.gov/.
          National Institutes of Health, Mammalian Gene Collection (MGC)
          Unpublished (1999)
          Contact: Robert Strausberg, Ph.D.
          Email: cgapbs-remail.nih.gov
          Tissue Procurement: ATCC
          cDNA Library Preparation: Ling Hong/Rubin Laboratory
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LLNL at:
          http://image.llnl.gov
          Plate: L1CM1220 row: k column: 24
          High quality sequence start: 4
          High quality sequence stop: 666.
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            /mol_type="mRNA"
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FEATURES
source
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/notes="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
 Site 2: EcoRI; cDNA made by oligo-dT priming
 Directionally, cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GCACACGAG) size-selected >500bp
 for average insert size 1.8kb. Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies). "

ORIGIN

Query Match	52.78; Score 631.4; DB 4; Length 856;
Best Local Similarity	91.5%; Pred. No. 1.7e-143;
Matches 783; Conservative	0; Mismatches 52; Indels 21; Gaps 10;
Qy	61 AAGCTTATCTGGTATTTAACTTTTCTTCTCTGCTCTCAAAATGAGAGTTAGATTTTATT 120
Db	854 AAGCTTATCTGGTATTTAAACTTTTCTTCTC--GCTCTCAAAATGAGAGTTAGATTTATT 797
Qy	121 TTTACATTTTCTAAGTGTCTGTCTCAT----GAAATCCTTCTATGGGGAAGC-T 175
Db	796 GTAACATGTCTAAGTGTCTCTGATTCGGCTCATGAAATCTTCTATGGGAAACCTT 737
Qy	176 GTGGGGCAGATTC--TTAAGCGACCTTTGGGACAACTC--TTATCAGGAGGAGGCGAA 231
Db	736 GTGGNGCAGATTCCTTTTAAACGACCCCTTTGGGACAACTCCTTATTACGGAGGAAACCGA 677
Qy	232 C---TGCTCATTTCTGCCTAC-TTCTTTTCCCTTCTGCT-TCACTGTACTACAAAA--- 288
Db	676 CTTGCTTCAATTTCTGCCTACTTCTTTCCCTTCTGCTGTATGTACTACCAAAATAG 617
Qy	283 TAGTCATTCGATGCAATGTGTGAGGCCCGCA-ATTAGGGAAGAAAGCTCTGGAAGCCCA 341
Db	616 TTCAATTTGCATGCAATTGGTGAGCCCGCACATTAGGGAAGAAAGCTCTGGAAGCCCA 557
Qy	342 TTTGCCATCTACACCTGTGTCAGGTCTTCAATTAATTTTGTGCACACGACAGAGGCTCTT 401
Db	556 TTTGCCATCTACACCTGTGTCAGGTCTTCAATTAATTTTGTGCCACGCCAGAGGCTCTT 497
Qy	402 TTGATTTTCCAAAATACAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGT 461
Db	496 TTGATTTTCCAAAATACAGGGAACCTCTTTTCCATGAGTACTCTCAGGTCTCTCTTTGT 437
Qy	462 TAAGTAGCTTTATCCCACGCAATTTGTGAAATGTAAACATCATGTGTTTCCATGGCGTG 521
Db	436 TAAGTAGCTTTATCCCACGCAATTTGTGAAATGTAAACATCATGTGTTTCCATGGCGTG 377
Qy	522 TTCCATTTGATATGGCAATTTTGTGTGGTCTGTTGAAGCCTTGCCGACGCGCGCGCAC 581
Db	376 TTCCATTTGATATGGCAATTTTGTGTGGTCTGTTGAAGCCTTGCCGACGCGCGCGCAC 317
Qy	582 GCTGGGCGAGCTGGGCGAGCTGGACGGGGCGGAGAGGCGCGCGGCTGTGCGC 641
Db	316 GCTGGGCGAGCTGGGCGAGCTGGACGGGGCGGAGAGGCGCGCGGCTGTGCGC 257
Qy	642 CTTCTTTAGTACGTGCGCGGGTGGGTAGAGGAGGCGGCGCGGAGCGGAGAGGCTGT 701
Db	256 CTTCTTTAGTACGTGCGCGGGTGGGTAGAGGAGGCGGTGCGGAGCGGAGAGGCTGT 197
Qy	702 GCGGGCGCTCGGCAGGGCGCTTCCCCAGCCCTGTCTCTCTCCCTTCTTCTGCCCCGAC 761
Db	196 GCGGGCGCTCGGCAGGGCGCTTCCCCAGCCCTGTCTCTCTCCCTTCTTCTGCCCCGAC 137
Qy	762 TCCCCGACCCCGGGCGGGCCACGCGCTGCCCTGCCGCGGACCGGCTCGCAGA 821
Db	136 TCCCCGACCCCGGGCGGGCCACGCGCTGCCCTGCCGCGGACCGGCTCGCAGA 77
Qy	822 GGCCTCGCCGCCCCACAGACAGAGGCTTCTGTAAACTTCTTTCAGTAGAAACGGTCTGT 881
Db	76 GGCCTCGCCGCCCCACAGACAGAGGCTTCTGTGTAACTTCTTTCAGTAGAAACGGTCTGT 17
Qy	882 CTCTCGAATATTTTCAAG 897
Db	16 CTCTCGAATATTTTCAAG 1

RESULT 26	ACCESSION	REFERENCE	JOURNAL
CA431436	VERSION	AUTHORS	COMMENT
LOCUS	KEYWORDS	TITLE	
DEFINITION	SOURCE		
	ORGANISM		

FEATURES
SOURCE

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Location/Qualifiers
1. .866
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/mol_type="mRNA"
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/clone="UI-H-FG1-bgp-m-06-0-UI"
/tissue_type="Cell lines"
/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP FG1"
/note="Organ: Enchondroma; Vector: pT7T3-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoK I; Site_2: Not I;
NCI CGAP FG1 is a normalized cDNA library obtained from a
pool of mRNA from 2 cell lines from Enchondroma tissues.
The library was constructed according to Bonaldo, Lennon
and Soares, Genome Research, 6:791-806, 1996. First strand
cDNA synthesis was primed with an oligo-dT primer
containing a Not I site. Double stranded cDNA was ligated
to an EcoR I adaptor, digested with Not I, and cloned
directionally into pT7T3-Pac vector. The oligonucleotide
used to prime the synthesis of first-strand cDNA contains
a library tag sequence that is located between the Not I
site and the (dT)18 tail. The sequence tag for this
library is CGGTCACTC. The cell lines were provided by Dr.
James Martin from the University of Iowa.
TAG TISSUE=Enchondroma cell line (Mix of EN1 and EN2)
TAG LIB=UI-H-FG1
TAG_SEQ=CGGTCACTC"

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ORIGIN

Query Match	52.6%	Score 630.8;	DB 6;	Length 666;
Best Local Similarity	99.5%;	Pred. No. 2.3e-143;		
Matches 643;	Conservative 0;	Mismatches 2;	Indels 1;	Gaps 1;

Qy	1	GGAACTAAAAAGAACTTTATTTATTCG-AGGGCAAGGGGATGCAACAATACAAAAATCA	59
Db	19	GGAACATAAAAAAGAACTTTATTTATTGNAGGCGAAGGGGATGCAACAATACAAAAATCA	78
Qy	60	AAAGCTTATCTGGTATTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT	119
Db	79	AAAGCTTATCTGGTATTAACTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT	138
Qy	120	TTTTACATTTGCTAAAGTGTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGG	179

Db 139 TTTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCTTCTATGCGGGAAGCTGTGG 198
 Qy 180 GGCAGATTCTTAAAGCAGCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 239
 Db 199 GGCAGATTCTTAAAGCAGCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 258
 Qy 240 TTTGCGCTACTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTGCATGCAAT 299
 Db 259 TTTGCGCTACTCTTTTCCCTTCTGCTTCATGTGTACTACAAAATAGTGCATGCAAT 318
 Qy 300 GGTGAGGCGCCCAATTAAGGAAAGAGAGCTCTGAAAGCCCACTTTGCCATCTCTACACTG 359
 Db 319 GGTGAGGCGCCCAATTAAGGAAAGAGAGCTCTGAAAGCCCACTTTGCCATCTCTACACTG 378
 Qy 360 GTCCAGGTCTCTTCAATTAATTTTGTCCACAGCAGAGGGTCTTTTGAATTTTCCAAAATCC 419
 Db 379 GTCCAGGTCTCTTCAATTAATTTTGTCCACAGCAGAGGGTCTTTTGAATTTTCCAAAATCC 438
 Qy 420 AGGAACTCTTTTCCATGAGTACTCTCAGTCTCTCTCTTTGTTAAGTAGCTTTATCCCC 479
 Db 439 AGGAACTCTTTTCCATGAGTACTCTCAGTCTCTCTCTTTGTTAAGTAGCTTTATCCCC 498
 Qy 480 AGCGAATTTGGAATGTAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAT 539
 Db 499 AGCGAATTTGGAATGTAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAT 558
 Qy 540 TTTGCTGTGTCCTTGAAGCTTTGGCGAGCGCGGCGAGCTGTGGCGAGCTGGGCGA 599
 Db 559 TTTGCTGTGTCCTTGAAGCTTTGGCGAGCGCGGCGAGCTGTGGCGAGCTGGGCGA 618
 Qy 600 GCTGAGCGCGGGCGGAGAGCGAGCGCGGCGGCTGTGCGCCCTC 645
 Db 619 GCTGAGCGCGGGCGGAAAGCGAGCGCGGCGGCTGTGCGCCCTC 664

RESULT 27
 BM546362/c
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 DEFINITION AGNCOURT 6498563 NIH_MGC_125 Homo sapiens cDNA clone IMAGE:5722924
 5', mRNA sequence.
 BM546362
 EST. BM546362.1 GI:18779258
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaps-remail.nih.gov
 Tissue Procurement: Invitrogen
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: L1AM12709 row: m column: 05
 High quality sequence stop: 616.

FEATURES

Location/Qualifiers
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 /clone="IMAGE:5722924"
 /lab_host="DH10B"
 /clone_lib="NIH_MGC_125"
 /note="Organ: ovary (pool of 3); Vector: pCMV-SPORT6;
 Site 1: EcoRV (destroyed); Site 2: NotI; RNA source pool
 of three ovaries, from females ranging in age from 38 to

49 yo. Library is oligo-dT primed and directionally cloned
 (EcoRV site is destroyed upon cloning). Average insert
 size 2.1 kb, insert size range 1-3.5 kb. Library is
 normalized and enriched for full-length clones and was
 constructed by C. Gruber (Invitrogen). Research Genetics
 tracking code 036."

ORIGIN

Query Match 52.5%; Score 629; DB 4; Length 687;
 Best Local Similarity 99.8%; Pred. No. 6.5e-143;
 Matches 640; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
 Qy 1 GGAACCTAAAAAGAAC-TTTTATTTATTTAGGCGCAAGGGGATGCAACAATACAAAAATCA 59
 Db 661 GGAACCTAAAAAGAAC-TTTTATTTATTTAGGCGCAAGGGGATGCAACAATACAAAAATCA 602
 Qy 60 AAAGCTTATCTGCTAATTAACCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 119
 Db 601 AAAGCTTATCTGCTAATTAACCTTTCTTCTCTGCTTGTCAAATGAGAGTTAGATTTTAT 542
 Qy 120 TTTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGGAAGCTGTGG 179
 Db 541 TTTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGGAAGCTGTGG 482
 Qy 180 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 239
 Db 481 GGCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGAGGAGCGAACTGCTCAT 422
 Qy 240 TTCTGCTACTTCTTCCCTTCTGCTTCTGCTCATGAAATGCTTCTATGAGATGCAAT 299
 Db 421 TTCTGCTACTTCTTCCCTTCTGCTTCTGCTCATGAAATGCTTCTATGAGATGCAAT 362
 Qy 300 GGTGAGGCGCGCAATTAGGAAAGAGCTCTGGAAGCCCACTTTTGGCACTCTCTACACTG 359
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 Qy 360 GTCCAGTCTCTTCAATTAATTTTGTCCACAGCAGAGGGTCTTTTGAATTTTCCAAAATCC 419
 Db 301 GTCCAGTCTCTTCAATTAATTTTGTCCACAGCAGAGGGTCTTTTGAATTTTCCAAAATCC 242
 Qy 420 AGGAACTCTTTTCCATGAGTACTCTCAGTCTCTCTTGTGTTAAGTAGCTTTATCCCC 479
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 Qy 480 AGCGAATTTCTGAAATGTAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAT 539
 Db 181 AGCGAATTTCTGAAATGTAACATCATGTTTCCATGCGGTGTTCCATTTGAGATGGCAT 122
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RESULT 28

BM546362/c
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 mRNA sequence.
 BM546362
 EST. BM546362.1 GI:11972219
 SOURCE
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCMI163 row: e column: 19
High quality sequence stop: 654.

FEATURES
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/mol_type="mRNA"
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/clone="IMAGE:4301946"
/tissue_type="leiomyosarcoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_46"
/note="Organ: uterus; Vector: pOTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

ORIGIN
Query Match 52.4%; Score 628.6; DB 2; Length 938;
Best Local Similarity 99.2%; Pred. No. 8.5e-143;
Matches 642; Conservative 0; Mismatches 4; Indels 1; Gaps 1;
Qy 1 GGAACTAAAAGAACTTTATTATTGAGGGCAAGGGATGCAACAATACAAAATCAA 60
Db 648 GAACCTAAAAGAACTTTATTATTGAGGGCAAGGGTATGCAACAATACAAAATCAA 589
Qy 61 AAGCTTATCTGGTATTTAACTTTTCTTCTGCTTGTCAAATCAGAGCTTAGATTTTATT 120
Db 588 AAGCTTATCTGGTATTTAACTTTTCTTCTGCTTGTCAAATCAGAGCTTAGATTTTATT 529
Qy 121 TTTACATTTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 180
Db 528 TTTACATTTGCTAAGTGCTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 469
Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAAT 240
Db 468 GCAGATTCCTTAAGCGACCCCTTTGGGACAACTCTTATCAGGGAGGAGCGAACTGCTCAAT 409
Qy 241 TCTGCCTACTTCTTTCCCTTCTGCTTCATGTGTACTAC-AAAATAGTCAATTGCATGCAT 299
Db 408 TCTGCCTACTTCTTTCCCTTCTGCTTCAGTGTACTACAAAAATAGTCATTTGCATGCAAT 349
Qy 300 GGTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 359
Db 348 GGTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 289
Qy 360 GTCCAGGTCCTTCAATATTATTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAAATCC 419
Db 288 GTCCAGGTCCTTCAATATTATTTGTCCACAGCAGAGGGTCTTTTGTATTTTCCAAAAATCC 229
Qy 420 AGGGAATCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGACCTTTATCCCC 479
Db 228 AGGGAATCCTTTTCCATGAGTACTCTCAGGTCCTCCTTTGTTAAGTAGACCTTTATCCCC 169
Qy 480 AGCGAAATTTGTGAATGTAAACATCATGGTTTCCATGGCGTGTTCCTATTGAGATGGCAT 539
Db 168 AGCGAAATTTGTGAATGTAAACATCATGGTTTCCATGGCGTGTTCCTATTGAGATGGCAT 109
Qy 540 TTTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGCGAGCGTGGCGAGCTGGGCGA 599

Db	108	TTTGGTGTGTCGTTGAAGCCTTGGCCGAGGCGCGGACACCTGGCGGAGTGTGGCGGA	49
Qy	600	GCTGGACGCGCGGCGGAGAGCGAGCGCGCGGCTGTGCGCTTCC	646
Db	48	GCTGGACGCGGCGGCGGAGAGCGAGCGCGGCGGCTGTGCGCTTCC	2
RESULT 29			
BE745512/c			
LOCUS	601579889F1 NIH_MGC_9	990 bp	mRNA linear EST 15-SEP-2000
DEFINITION	601579889F1 NIH_MGC_9 Homo sapiens cDNA clone IMAGE:3928606 5', mRNA sequence.		
ACCESSION	BE745512		
VERSION	BE745512.1	GI:10159504	
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 990)		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs-x@mail.nih.gov Tissue Procurement: DCTD/DTF cDNA Library Preparation: Ling Hong/Rubin Laboratory cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: image.llnl.gov Plate: L1CM760 row: a column: 23 High quality sequence stop: 650.		
FEATURES	Location/Qualifiers		
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	/organism="Homo sapiens"		
	/mol_type="mRNA"		
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	/clone="IMAGE:3928606"		
	/tissue_type="adenocarcinoma cell line"		
	/lab_host="DH10B (phage-resistant)"		
	/clone_lib="NIH_MGC_9"		
	/note="Organ: ovary; Vector: pOTB7; Site 1: XhoI; Site 2: EcoRI; cDNA made by oligo-dT priming. Directionally cloned into EcoRI/XhoI sites using the following 5' adaptor: GGCACGAG(G). Size-selected >500bp for average insert size 1.8kb. Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies)."		
ORIGIN			
Query Match	52.4%	Score 628.6;	DB 2; Length 990;
Best Local Similarity	99.4%	Pred. No. 8.6e-143;	
Matches 631;	Conservative	0; Mismatches 4;	Indels 0; Gaps 0;
Qy	1	GGAACTAAAAAGAACTTTATTTATTGAGGCGCAAGGGGATGCAAAACAATAACAAAAATCAA	60
Db	635	GGAACTAAAAAGAACTTTATTTATTGAGGCGCAAGGGGATGCAAAACAATAACAAAAATCAA	576
Qy	61	AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGTGTCAAAATGAGAGTTAGATTTTATT	120
Db	575	AAGCTTATCTGGTATTTAACTTTTCTTTCTCTGTGTCAAAATGAGAGTTAGATTTTATT	516
Qy	121	TTTACATTTGCTAAGTGTCTGATCTGCTCATGAATCTTCTATGGGGAAGCTGTGGG	180
Db	515	TTTACATTTGCTAAGTGTCTGATCTGCTCATGAATCTTCTATGGGGAAGCTGTGGG	456
Qy	181	GCAGATTCTTTAAGCGACCCCTTTTGGGACAACTCTTTATCAGGAGGAGCGCAACTGCTCAT	240
Db	455	GCAGATTCTTTAAGCGACCCCTTTTGGGACAACTCTTTATCAGGAGGAGCGCAACTGCTCAT	396
Qy	241	TCTGCCTACTCTTTTCCCTTTCTGCTTCATGTACTACAAATAGTCAATTGCAATGCAATG	300

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Db      395  TCTGCTACTTCTTCCCTTCTGCTTCATGTGTAAGTACAAATAGTCAATGCATGCAATG 336
Qy      301  GTGAGGCCGCAATTAGGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db      335  GTGAGGCCGCAATTAGGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTAG 276
Qy      361  TCCAGGCTCTTCATATTTTGTCCACACAGAGAGGCTCTTTTGTATTTCCAAAATCCA 420
Db      275  TCCAGGCTCTTCATATTTTGTCCACACAGAGAGGCTCTTTTGTATTTCCAAAATCCA 216
Qy      421  GCGAACTCTTTTCCATGACTCTCAGGTCTCTCTTTGTAAAGTACGCTTTATCCCA 480
Db      215  GCGAACTCTTTTCCATGACTCTCAGGTCTCTCTTTGTAAAGTACGCTTTATCCCA 156
Qy      481  GCGAAATTTGTAATGTAATCATCATGTTTCCATGCGTGTCCATTTGAGATGGCAAT 540
Db      155  GCGAAATTTGTAATGTAATCATCATGTTTCCATGCGTGTCCATTTGAGATGGCAAT 96
Qy      541  TTGCTGTGCTCGTTCAGGCTTTGGCCAGAGCGGCGGAGCTGGGCGAGCTGGGCGAG 600
Db      95  TTGCTGTGCTCGTTCAGGCTTTGGCCAGAGCGGCGGAGCTGGGCGAGCTGGGCGAG 36
Qy      601  CTGACGCGGCGGCGAGAGCGGCGGCGGCGGCT 635
Db      35  CTGACGCGGCGGCGAGAGCGGCGGCGGCT 1

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RESULT 30
BI858258/6
LOCUS
DEFINITION 603384021P1 NIH_MGC_87 Homo sapiens cDNA clone IMAGE:532973 5',
mRNA sequence.
ACCESSION BI858258
VERSION
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: DCTD/BTP
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: L14M12001 Row: i column: 06
High quality sequence stop: 663.
Location/Qualifiers
1..674
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:532973"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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FEATURES

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source
1..674
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:532973"
/tissue_type="mammary adenocarcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC 87"
/note="Organ: breast; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.383 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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ORIGIN

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Query Match 52.4%; Score 628.4; DB 4; Length 674;
Best Local Similarity 99.5%; Pred. No. 9.1e-143;

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Matches 651; Conservative 0; Mismatches 1; Indels 2; Gaps 2;
Qy      1  GGAACTAAAAAGAACTTTATTTATGAGGCAAGGGAGTCAAAACAATAC-AAATAATCA 59
Db      654  GGAACTAAAAAGAACTTTATTTATGAGGCAAGGGAGTCAAAACAATACCGGAAATCA 595
Qy      60  AAAGCTTATCTGGTATTTAACTTTTCTCTCTGCTGTCAATGAGAGTTAGATTTAT 119
Db      594  AAAGCTTATCTGGTATTTAACTTTTCTCTCTGCTGTCAATGAGAGTTAGATTTAT 535
Qy      120  TTTTACATTTGCTAAGTGTCTGATCTGCTCAATCAAAATCTTCTATGGGGAAGCTGGG 179
Db      534  TTTTACATTTGCTAAGTGTCTGATCTGCTCATGAAATCTTCTATGGGGAAGCTGGG 475
Qy      180  GGCAGATTCCTTAAGCACCCTTTGGGCAACTCTTATCAGGGAGGAGCGAACTGCTCAT 239
Db      474  GGCAGATTCCTTAAGCACCCTTTGGGCAACTCTTATCAGGGAGGAGCGAACTGCTCAT 415
Qy      240  TTCTGCTTACTTCTTCCCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 299
Db      414  TTCTGCTTACTTCTTCCCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 355
Qy      300  GGTGAGGCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 359
Db      354  GGTGAGGCCGCAATTAGGGAAGAAAGCTCTGGAAGCCCACTTTGCCATCTCTACACTG 295
Qy      360  GTCCAGGTCTCTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCC 419
Db      294  GTCCAGGTCTCTCATTTATTTGTCCACAGCCAGAGGGTCTTTTGTATTTTCCAAAATCC 235
Qy      420  AGGGAATCTCTTTTCCATGAGTA-CTCTCAGGTCTCTCTTTGTTAAGTAGCTTTATCCC 478
Db      234  AGGGAATCTCTTTTCCATGAGTAGTCTCTCAGGTCTCTCTTTGTTAAGTAGCTTTATCCC 175
Qy      479  CAGCGAATTTGTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCA 538
Db      174  CAGCGAATTTGTGAAATGTAACATCATGTTTCCATGGCGTGTTCATTTGAGATGGCA 115
Qy      539  TTTTGTGTGCTCGTTCGTTGAAGCTTTGGCCAGGCGCGGCGGAGCTGGGAGCTGGGCG 598
Db      114  TTTTGTGTGCTCGTTCGTTGAAGCTTTGGCCAGGCGCGGCGGAGCTGGGAGCTGGGCG 55
Qy      599  AGCTGGAGCGGCGGCGGAGGCGGCGGCGGCTGTGGCGCTTCTTAGTA 652
Db      54  AGCTGGAGCGGCGGCGGAGGCGGCGGCGGCTGTGGCGCTTCTTAGTA 1

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RESULT 31

CA307888

LOCUS

DEFINITION

UI-H-FT1-bib-a-01-0-UI.s1 NCI CGAP FT1 Homo sapiens cDNA clone

UI-H-FT1-bib-a-01-0-UI 3', mRNA sequence.

ACCESSION

CA307888

VERSION

CA307888.1 GI:24470942

KEYWORDS

EST.

SOURCE

Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

1 (bases 1 to 686)

AUTHORS

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

JOURNAL

Unpublished (1997)

COMMENT

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

CDNA Library Preparation: Dr. Gary W. Hunninghake, U of I

CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Clone distribution information can be obtained

from Dr. M. Bento Soares, bento-soares@uiowa.edu

Seq primer: M13 FORWARD

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POLYA=Yes.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /c1ones="UI-H-FT1-bib-a-01-0-UI"
                     /tissue_types="Alveolar Macrophage"
                     /dev_stage="Adult"
                     /lab_host="DH10B (Life Technologies)"
                     /clone_lib="NCI CGAP Ftl1"
                     /notes="Organ: Lung; Vector: p7T3-Pac (Pharmacia) with a
                     modified polylinker; Site 1: EcoR I; Site 2: Not I;
                     NCI CGAP Ftl1 is a normalized cDNA library constructed from
                     a pool of 81 RNA samples from Alveolar Macrophages
                     challenged with different treatments. The mRNA samples
                     were a mixture of these conditions (times refer to
                     incubations following isolation by bronchoalveolar lavage)
                     (some normal donor macrophages were cultured in some of
                     the conditions, other donor macrophages in different
                     conditions). The mRNA samples were pooled for library
                     construction. Control 0 hours; control 3 hours; control 24
                     hours; LPS 100 ng/ml, 3 hours; LPS 100 ng/ml, 24 hours;
                     PMA 10 ng/ml, 3 hours; PMA 10 ng/ml, 24 hours; Klebsiella
                     moi 10, 3 hours; Klebsiella moi 10, 24 hours; Staph aureus
                     moi 10, 3 hours; Staph aureus moi 10, 24 hours; Adenoviral
                     vector (Ad5 CMV eGFP), moi 500, 3 hours; Adenoviral vector
                     (Ad5 CMV eGFP), moi 500, 24 hours; wt adenovirus moi 500,
                     3 hours; wt adenovirus moi 500, 24 hours; Ad vector + LPS
                     3 hours; Ad vector + LPS 24 hours; wt adenovirus + LPS 3
                     hours; wt adenovirus + LPS 24 hours. The library was
                     normalized according to Bonaldo, Lennon and Soares, Genome
                     Research, 6:791-806, 1996. First strand cDNA synthesis was
                     primed with an oligo-dT primer containing a Not I site.
                     Double stranded cDNA was ligated to an EcoR I adaptor,
                     digested with Not I, and cloned directionally into
                     pT73-pac vector. The oligonucleotide used to prime the
                     synthesis of first-strand cDNA contains a library tag
                     sequence that is located between the Not I site and the
                     (dfl)18 tail. The sequence tag for this library is
                     GGCCATGCCG. The tissue was provided by Dr. Gary W.
                     Hunninghake of the University of Iowa.
                     TAG TISSUE=Human Lung Alveolar Macrophage
                     TAG LIB=UI-H-FT1
                     TAG_SEQ=GGCCATGCCG"

ORIGIN
Query Match      52.4%; Score 628.2; DB 6; Length 686;
Best Local Similarity 99.2%; Pred. No. 1e-142;
Matches 652; Conservative 0; Mismatches 3; Indels 2; Gaps 2;

Qy 1 GGAACATAAAGAACCTTTATTTAGGGCAAGGGATGCAACAACTACAAAATCAA 60
Db 19 GGAACATAAAGAACCTTTATTTAGGGCAAGGGATGCAACAACTACAAAATCAA 78
Qy 61 AAGCTTATCTGGTATTTAACTTTCTTCTGCTCTGCTCAAAATGAGAGTTAGATTTTATT 120
Db 79 AAGCTTATCTGGTATTTAACTTTCTTCTGCTCTGCTCAAAATGAGAGTTAGATTTTATT 138
Qy 121 TTATCATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGAAGCTGTGGG 180
Db 139 TTATCATTTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGAAGCTGTGGG 198
Qy 181 GCAGATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGACGCACTGCTCATTT 240
Db 199 GCAAAATTCCTTAAGCGACCCCTTTGGGCAACTCTTATCAGGAGGACGCACTGCTCATTT 258
Qy 241 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTCGATGCAATG 300
Db 259 TCTGCCTACTTCTTCCCTTCTGCTTCATGTGTACTACAAAATAGTCAATTCGATGCAATG 318
Qy 301 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360

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Db 319 GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 378
Qy 361 TCCAGGTCTCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTCCTCAAAAATCCA 420
Db 379 TCCAGGTCTCTTCATTATTTTGTCCACAGCCAGAGGGTCTTTTTCATTTCCTCAAAAATCCA 438
Qy 421 GGGAACTCTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTTTGTTAAGTAGCCCTTTATCCCCA 480
Db 439 GGGAACTCTCTTTTCCATGAGTACTCTCAGGTCTCTCTCTTTGTTAAGTAGCCCTTTATCCCCA 498
Qy 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGGCAATT 540
Db 499 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGG-ATT 557
Qy 541 TTGGTGTGTCCTTGAAGCCTTTGGCCGAGGCGGCGGAGCGCTGGCGAGCTGGGCGAG 600
Db 558 TTGGTGTGTCCTTGAAGCCTTTGGCCGAGGCGGCGGAGCGCTGGCGAGCTGGGCGAG 617
Qy 601 CTGAGCGCGGGCGGAGAGCGGCGGCGGCTGTGCGCCCTTCTCTTACTAGCTGC 657
Db 618 CTGAGCGCGGGCGGAGAAAGCGGAGCGGCGGCTGTGCG-CTTCTTAGTAGCTGC 673

RESULT 32
BI488419/c
LOCUS      BI488419.1 811 bp mRNA linear EST 28-AUG-2001
DEFINITION mRNA sequence.
ACCESSION BI488419
VERSION   BI488419.1 GI:15327647
KEYWORDS  EST.
SOURCE    Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 811)
AUTHORS  NIH-MGC http://mgc.nci.nih.gov/.
TITLE    National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL  Unpublished (1999)
COMMENT  Contact: Robert Strausberg, Ph.D.
          Email: cgabs-k@mail.nih.gov
          Tissue Procurement: Life Technologies, Inc.
          cDNA Library Preparation: Life Technologies, Inc.
          cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
          DNA Sequencing by: Incyte Genomics, Inc.
          Clone distribution: MGC clone distribution information can be
          found through the I.M.A.G.E. Consortium/LNL at:
          http://image.llnl.gov
          Plate: L1AM11479 row: a column: 05
          High quality sequence stop: 669.

FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_114"
                     /notes="Organ: Brain; Vector: pCMV-SPORT6; Site 1: NotI;
                     Site 2: EcoRV (destroyed); RNA source anonymous pool of 6
                     male brains, age range 23-27 yo. Library is oligo-dT
                     primed and directionally cloned (EcoRV site is destroyed
                     upon cloning). Average insert size 1.5 kb, insert size
                     range 1-3 kb. Library is normalized and enriched for
                     full-length clones and was constructed by C. Gruber
                     (Invitrogen). Research Genetics tracking code 019. Note:
                     this is a NIH_MGC Library."

ORIGIN
Query Match      52.4%; Score 627.8; DB 4; Length 811;
Best Local Similarity 98.2%; Pred. No. 1.3e-142;
Matches 659; Conservative 0; Mismatches 2; Indels 10; Gaps 2;

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Qy 1 GGAACCTAAAGAACTTTATTTATGAGGCAAGGGATGCAACAATACAAAATCAA 60
Db 671 GGAACCTAAAGAACTTTATTTATGAGGCAAGGGATGCAACAATACAAAATCAA 612
Qy 61 AAGCTTATCTGCTATTTAACTTTCTCTCTCTGCTGTCAATGAGAGCTAGATTTTAT 120
Db 611 AAGCTTATCTGCTATTTAACTTTCTCTCTCTGCTGTCAATGAGAGCTAGATTTTAT 552
Qy 121 TTTACATTTGCTAAGTCTGCTGATCTGCTCATGAATCTTTCTATGAGGGAAGCTGTGG 180
Db 551 TTGACATTTGCTAAGTCTGCTGATCTGCTCATGAATCTTTCTATGAGGGAAGCTGTGG 492
Qy 181 CGAGATTTCTTAAAGGACCTTTGGGCAACTTTATCAGGAGGAGGAACTGCTCAT 240
Db 491 CGAGATTTCTTAAAGGACCTTTGGGCAACTTTATCAGGAGGAGGAACTGCTCAT 432
Qy 241 TCTGCTACTTCTTTCCCTCTCTGCTTCAATGCTACTACAAATAGTCAATGCATGCAATG 300
Db 431 TCTGCTACTTCTTTCCCTCTCTGCTTCAATGCTACTACAAATAGTCAATGCATGCAATG 372
Qy 301 GTGAGGCGCGCAATTTAGGAAAGAAAGCTTGGAGGCCACTTTGCCATCTCTACACTGG 360
Db 371 GTGAGGCGCGCAATTTAGGAAAGAAAGCTTGGAGGCCACTTTGCCATCTCTACACTGG 312
Qy 361 TCCAGGCTCTCATATTTTGTGCACAGCCAGAGGCTTTTGTGATTTTCCAAAATCCA 420
Db 311 TCCAGGCTCTCATATTTTGTGCACAGCCAGAGGCTTTTGTGATTTTCCAAAATCCA 252
Qy 421 GGGAACTCTTT-TTCCATGACTCTCTCAGTCTCTCTCTGCTTAAAGTAGCCTTTATCCCC 479
Db 251 GGGAACTCTTTTCTCATGAGTCTCTCAGTCTCTCTCTGCTTAAAGTAGCCTTTATCCCC 192
Qy 480 AGCGAATTTGCAATGTAAACATCATGTTTCCATGCGCTGTTCCTATTTGAGATGGCAT 539
Db 191 AGCGAATTTGCAATGTAAACATCATGTTTCCATGCGCTGTTCCTATTTGAGATGGCAT 132
Qy 540 TTTGGTGTGCTCGTTGAAGCTTTGGCGAGCGCGCGGCGAC-----GCTGGCGGA 590
Db 131 TTTGGTGTGCTCGTTGAAGCTTTGGCGAGCGCGCGGCGACGCTGGCGGAGCTGGCGGA 72
Qy 591 GCTGGGCGAGCTGGAGCGGGGCGAGAGGCGGCGGCGGCTGTGCGGCTTCTTAG 650
Db 71 GCTGGGCGAGCTGGAGCGGGGCGAGAGGCGGCGGCGGCTGTGCGGCTTCTTAG 12
Qy 651 TACGTGCGGCG 661
Db 11 TACGTGCGGCG 1

RESULT 33
CA412335
LOCUS
DEFINITION
UI-H-E20-bak-j-10-0-UI.s1 NCI CGAP Ch1 Homo sapiens cDNA clone
UI-H-E20-bak-j-10-0-UI 3', mRNA sequence.
CA412335
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 665)
NCI-Genes http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Steven Gitelis/ Rush Presbiterian, Dept. of
Orthopedics
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
```

Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
Seq primer: M13 FORWARD
POLYA=Yes

FEATURES

source

Location/Qualifiers
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/db_xref="taxon:9606"
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/dev_stage="Adult"
/lab_host="DH10B (Life Technologies)"
/clone_lib="NCI CGAP Ch1"
/note="Organ: Left Pelvis; Vector: pT7T3-Pac (Pharmacia) with a modified polylinker; Site 1: EcoR I; Site 2: Not I; NCI CGAP Ch1 is a cDNA library containing the following tissue(s): Chondrosarcoma Grade II. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pT7T3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (dT)18 tail. The sequence tag for this library is TGATCAGCT.
TAG_TISSUE=grade-2-chondrosarcoma
TAG_LIB=UI-H-E20
TAG_SEQ=ATCTAATATG"

ORIGIN

Query Match 52.3%; Score 627; DB 6; Length 665;
Best Local Similarity 99.1%; Pred. No. 2e-142;
Matches 641; Conservative 0; Mismatches 5; Indels 1; Gaps 1;
Qy 1 GGAACCTAAAGAACTTTATTTAT-TGAGGCGCAAGGGATGCAACAATACAAAATCAA 59
Db 19 GGAACCTAAAGAACTTTATTTATNTAGGCGCAAGGGATGCAACAATACAAAATCAA 78
Qy 60 AAGCTTATCTGCTATTTAACTTTCTCTCTGCTGTCAAAATGAGAGTTAGATTTTAT 119
Db 79 AAGCTTATCTGCTATTTAACTTTCTCTCTGCTGTCAAAATGAGAGTTAGATTTTAT 138
Qy 120 TTTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCTCTTATCGGGGAAGCTGG 179
Db 139 TTTTACATTTGCTAAGTCTCTGATCTGCTCATGAAATCTCTTATGGGGAAGCTGG 198
Qy 180 GGCAGATTCTTAAAGCGACCTTTTGGGCAACTCTTATCAGGAGGAGCGAACTGCTCAT 239
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Qy 240 TTCTGCTACTCTCTTCCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 299
Db 259 TTCTGCTACTCTCTTCCCTTCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 318
Qy 300 GGTGAGGCGCGCAATTTAGGGAAGAGCTCTGGAAGCCCACTTTGCGCATCTCTACACTG 359
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Qy 360 GTCCAGGCTCTTCAATTTATTTGTCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCC 419
Db 379 GTCCAGGCTCTTCAATTTATTTGTCACAGCAGAGGCTCTTTTGTATTTTCCAAAATCC 438
Qy 420 AGGGAATCTCTTTTCCATAGTACTCTCAGGCTCTCTTCTTGTAAAGTAGCTTTATCCCC 479
Db 439 AGGGAATCTCTTTTCCATAGTACTCTCAGGCTCTCTTCTTGTAAAGTAGCTTTATCCCC 498
Qy 480 AGCGAATTTGAAATGTAAACATCATGTTTCCATGGCGCTGTCCATTTGAGATGGCAT 539
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QY 540 TTTGGTGTGTCCTTGAACCTTGGCCGAGCGCGCGAGCGCTGGCGAGCTGGGCGGA 599
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QY 600 GCTGGAGCGGGGCGGAGAGCGCGCGCGGGCTGTGCGCCTTCC 646
Db 619 GCTGGACCGGAGCGGATAGCGAGCGCGCGGGCTGTGCGCCTTCC 665

RESULT 34
AI749536
LOCUS
DEFINITION
  at30806.x1 Barstead colon HPLRB7 Homo sapiens cDNA clone
  IMAGE:2373491 3' similar to gb:M38591 CALPACTIN I LIGHT CHAIN
  (HUMAN);, mRNA sequence.
ACCESSION
  AI749536
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 641)
  Hallier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S.,
  Krizman,D., Kucaba,T., Lacy,M., Lennon,G., Marra,M.,
  Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F.,
  Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
  WashU-NCI human EST Project
  Unpublished (1997)
  Contact: Wilson RK
  Washington University School of Medicine
  4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
  Tel: 314 286 1800
  Fax: 314 286 1810
  Email: est@watson.wustl.edu
  This clone is available royalty-free through LLNL ; contact the
  IMAGE Consortium (info@image.llnl.gov) for further information.
  Seq primer: -40UP from Gibco
  High quality sequence stop: 470.
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      /clone_lib="Barstead colon HPLRB7"
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      TGTTAGCACTGAAGTGGAGCGCGCCCTTTTTTTTTTTTTTTTTTTTTT
      3']; double-stranded cDNA was ligated to Eco RI adaptors
      [5', AATTACTAGTAAT 3' and 5' ATTACTAGT 3'], digested
      with Not I and cloned into the Not I and Eco RI sites of
      the modified pT7T3 vector. Library constructed by Bob
      Barstead."

ORIGIN
  Query Match 52.2%; Score 626.4; DB 1; Length 641;
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QY 1 GGAACATAAAAGAACCTTTATTATTGAGGCGAAGGGATGCAAAACAATACAAAATCAA 60
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QY 61 AAGCTATCTGGTATTAACTTTCTCTCTGCTCAATGACAGAGTTAGATTTATT 120
Db 64 AAGCTATCTGGTATTAACTTTCTCTCTGCTCAATGACAGAGTTAGATTTATT 123
QY 121 TTTACATTTGCTAAGTGTCTCGTCTGCTCATGAAATCTCTTCTATGGGGGAGCTGTGGG 180
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Db 244 TCTGCCCTACTCTTCTTCCCTTCTGCTTCACTGTACTACAAAATAGTCAATTGCAATG 303
QY 301 GTGAGCCCGCAATTAGGGAAGAAGCTCTTGAAGCCCACTTTGGCATCTCTTACACTGG 360
Db 304 GTGAGCCCGCAATTAGGGAAGAAGCTCTTGAAGCCCACTTTGGCATCTCTTACACTGG 363
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QY 421 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTTAAGTAGCCTTTATCCCCA 480
Db 424 GGGAACTCCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTTAAGTAGCCTTTATCCCCA 483
QY 481 GCGAATTTGTGAATGTAAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGCGATT 540
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Db 544 NTGGTGTGTCGTTGAAAGCCTTGGCGGAGCTGGCGGAGCGCGCTGGCGAGCTGGGCGAG 603
QY 601 CTGGACGCGGGCGGAGAGCGAGCGCGCGGCTGTG 638
Db 604 CTGGACGCGGGCGGAGAGCGCGCGGCTGTG 641

BQ948995 641 bp mRNA linear EST 21-AUG-2002
AGENCOURT_8912008 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:6464957
5', mRNA sequence.
ACCESSION BQ948995
VERSION BQ948995.1 GI:22364473
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 641)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: ATCC
cDNA Library preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM13986 row: 0 column: 06
High quality sequence stop: 640.
Location/Qualifiers
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    /clone_lib="NIH MGC 71"
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DEFINITION 1700600075087 GRN_PNEU Homo sapiens cDNA 5', mRNA sequence.
ACCESSION  CN271600
VERSION     CN271600.1  GI:47288014
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1  (bases 1 to 637)
AUTHORS     Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Fisk,G.J.,
              Li,Y., Xu,C., Pang,R., Guegler,K., Rao,M.S., Mandalam,R.,
              Lebkowski,J and Stanton,L.W.
TITLE       Transcriptome characterization elucidates signaling networks that
JOURNAL     Nat. Biotechnol. 22 (6), 707-716 (2004)
COMMENT     Contact: Brandenberger R
              Regenerative Medicine
              Genon Corporation
              230 Constitution Drive, Menlo Park, CA 94025, USA
              Tel: 650 473 8658
              Fax: 650 473 7760
              Email: rbrandenberger@genon.com
              Insert Length: 637 Std Error: 0.00.
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                /notes="oligo dt primed, full-length enriched cDNA library
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ORIGIN
Query Match      51.9%; Score 622.8; DB 7; Length 637;
Best Local Similarity 99.7%; Pred. No. 2.1e-141;
Matches 624; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1  GGAACAAAAAGAACCTTTATTATTCAGGCGCAAGGGGATGCAAAACAATACAAAAATCAA 60
Db 626  GGAACAAAAAGAACCTTTATTATTCAGGCGCAAGGGGATGCAAAACAATACAAAAATCAA 567
Qy 61  AAGCTTATCTGGTATTAACTTTTCTCTGCTGTCGCAAAATGAGAGTTAGATTTTATT 120
Db 566  AAGCTTATCTGGTATTAACTTTTCTCTGCTGTCGCAAAATGAGAGTTAGATTTTATT 507
Qy 121  TTTACATTGCTAAGTGTCTGATCTGCTCATGAAATCCTTTCTATGGGGGAAGCTGTGGG 180
Db 506  TTTACATTGCTAAGTGTCTGATCTGCTCATGAAATCCTTCTATGGGGGAAGCTGTGGG 447
Qy 181  GCAGATTCTTAAGCGACCCCTTTGGGCAACTCTTTATCAGGGAGGACGAACCTCTCATTT 240
Db 446  GCAGATTCTTAAGCGACCCCTTTGGGCAACTCTTTATCAGGGAGGACGAACCTCTCATTT 387
Qy 241  TCTGCCCTACTCTTTTCCCTCTGCTTCTATGCTGTAACAAAATAGTCAATTCATGCAATG 300
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Qy 301  GTGAGGCCCGCAATTAGGAAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 360
Db 326  GTGAGGCCCGCAATTAGGAAAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG 267
Qy 361  TCCAGGTCCTTCATTATTATTTGTCACAGCAGAGGGTCTTTTGTGATTTTCCAAAAATCCA 420
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Qy 481  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGCGTGTCCCATTTGAGATGGCAATT 540
Db 146  GCGAATTTGTGAAATGTAAACATCATGGTTTCCATGCGCGTGTCCCATTTGAGATGGCAATT 87
Qy 541  TTGGTGTGTCCTTGAAGCCTTGGCGAGCGCGGGACGCTGGCGAGCTGGCGGAG 600
Db 86  TTGGTGTGTCCTTGAAGCCTTGGCGAGCGCGGGACGCTGGCGAGCTGGCGGAG 27
Qy 601  CTGGACGCGGGCGGAGAGCGGAGCG 626
Db 26  CTGGACGCGGGCGGAGAGCGGAGCG 1
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BM767559/c
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DEFINITION K-EST0050042 S1SNU5s2 Homo sapiens cDNA clone S1SNU5s2-3-G06 5',
              mRNA sequence.
ACCESSION  BM767559
VERSION     BM767559.1  GI:19097174
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
REFERENCE   1  (bases 1 to 625)
AUTHORS     Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
              Mammalia; Eutheria; Primates; Catarhini; Homnidae; Homo.
              Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.,
              Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and
              Kim,Y.S.
TITLE       21C Frontier Korean EST Project 2001
JOURNAL     Unpublished (2002)
COMMENT     Contact: Kim YS
              Genome Research Center
              Korea Research Institute of Bioscience & Biotechnology
              52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
              Tel: +82-42-860-4470
              Fax: +82-42-860-4409
              Email: yongsung@mail.kribb.re.kr
              Plate: 3 row: G column: 06
              High quality sequence stop: 625.
FEATURES    Location/Qualifiers
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                /lab_host="Top10F"
                /clone_lib="S1SNU5s2"
                /note="Organ: Stomach; Vector: pcNS; Site_1: EcoRI;
                Site_2: NotI; The poly (A)+ RNA was dephosphorylated with
                bacterial alkaline phosphatase (BAP) and then decapped
                with tabacco acid pyrophosphatase (TAP). The decapped
                intact mRNA was ligated with DNA-RNA linker including EcoR
                I site by treatment of T4 RNA ligase and the first strand
                cDNA was synthesized from oligo dt-selected mRNA by
                priming with dt-tailed vector. The dt-tailed vector was
                adjusted to have about 60nt. The cDNA vector was
                circularized with E. coli DNA ligase after digestion of
                EcoRI which site is also included in vector. An RNA strand
                converted to a DNA strand by Okayama-Berg method. The
                obtained cDNA vectors were used for transformation of
                competent cells E. coli Top10F by electroporation method.
                The cDNA libraries constructed by this method are
                full-length enriched cDNA library. After analyzing and
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Db	323	GTGAGGCCCAATTAGGGAAGAAGCTCGAAGCCCACTTGGCATCTCTACACTGG	264
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Qy	421	GGGAATCTCTTTCCATGAGTACTCTCAGTCTCTCTTGTAAAGTAGCCTTTATCCCCA	480
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Qy	481	GCGAATTTGGAATGAAACATCATGTTTCCATGCGGTGTTCCATTTCAGATGGCAAT	540
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Db	83	TTGGTGTGGTCCGTGGAAGCCTTGGCCGAGCGCGGAGCGCTGGCGAGCTGGCGGAG	24
Qy	601	CTGGACGCGGGCGGAGAGCGA	623
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LOCUS			
DEFINITION	BU860855 794 bp mRNA linear EST 16-OCT-2002		
ACCESSION	AGENCOURT 10435041 NIH_MGC_126 Homo sapiens cDNA clone		
VERSION	IMAGE:6652090 5', mRNA sequence.		
KEYWORDS	EST.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 794)		
COMMENT	NIH-MGC http://mgi.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs@mail.nih.gov		
	Tissue Procurement: NCI		
	cDNA Library Preparation: Michael Brownstein Laboratory		
	cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: Agencourt Bioscience Corporation		
	Clone distribution: MGC clone distribution information can be		
	found through the I.M.A.G.E. Consortium/LLNL at:		
	http://image.llnl.gov		
	Plate: LLCM2899 row: p column: 10		
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	/clone_lib="NIH_MGC_126"		
	/notes="Vector: pDNR-LIB; Site 1: SfiI (ggccattatggcc);		
	Site 2: SfiI (ggccgctcgcc); Double-stranded cDNA was		
	prepared from a pool of 40 cell line polyA+ RNAs (bladder		
	- 2%, blood - 33.4%, brain - 5.6%, breast - 12.5%, colon -		
	4%, connective tissue - 1.4%, eye - 1%, intestine - 2.6%,		
	kidney - 2.2%, liver - 5.7%, lung - 10.8%, NK-cell -		
	5.2%, ovary - 4%, pharynx - 2.5%, prostate - 4.3%,		
	salivary gland - 1.3%, and skin - 2.3%). 5' and 3'		
	adaptors were used in cloning as follows:		
	5'-AACGATGGTATCAACGATGGCATACGCGGG-3' and		
	5'-ATTCTAGACCGGCGGCGGACATG-dt(30)NN-3'. Full-length		
	enriched library was constructed using the Clontech		
	Creator SMART kit and size-selected to contain the 0.5-1		

kb size fraction (other fractions present in NIH_MGC 127 and NIH_MGC 128). Library created in the laboratory of T. Usdin, M.D., Ph.D. (NIMH, NIH). Note: this is a NIH_MGC Library."			
ORIGIN			
Query Match	51.8%;	Score 621;	DB 5; Length 794;
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Matches 621;	Conservative 0;	Mismatches 0;	Indels 0; Gaps 0;
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Qy	61	AGCTTATCTGGTATTAACTTTCTCTCTCTGTCAATGAGAGTTAGATTTATT	120
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Qy	121	TTTACATTTGCTAAAGTGTCTGATCTGCTCATGAAATCTCTTATGGGGAAGCTGTGGG	180
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Qy	301	GTGAGGCCCGCAATTAGGGAAGAAAGAGCTCTGGAAGCCCACTTTGCCATCTCTACACTGG	360
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Qy	361	TCAGAGTCTCTCAATATTTTGTGCCAGCCAGAGGGTCTTTTGTATTTCCAAAATCCA	420
Db	264	TCAGAGTCTCTCAATATTTTGTGCCAGCCAGAGGGTCTTTTGTATTTCCAAAATCCA	205
Qy	421	GGGAATCTCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTTAAAGTAGCCTTTATCCCCA	480
Db	204	GGGAATCTCTTTTCCATGAGTACTCTCAGTCTCTCTTTGTTAAAGTAGCCTTTATCCCCA	145
Qy	481	GCGAATTTGTGAATTAACATCATGTTTCCATGCGGTGTTTCCATTTGAGATGGCAAT	540
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Db	84	TTGGTGTGGTCCGTTGAAGCCTTTGGCCGAGCGCGGAGCGCTGGCGAGCTGGCGGAG	25
Qy	601	CTGGACGCGGGCGGAGAGGC	621
Db	24	CTGGACGCGGGCGGAGAGGC	4
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LOCUS			
DEFINITION	BO943717 638 bp mRNA linear EST 21-AUG-2002		
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SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE			
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 638)		
COMMENT	NIH-MGC http://mgi.nci.nih.gov/.		
	National Institutes of Health, Mammalian Gene Collection (MGC)		
	Unpublished (1999)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgabbs@mail.nih.gov		

Tissue Procurement: DCTD/DTP
 cDNA Library Preparation: Rubin Laboratory
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLM2580 row: 9 column: 04
 High quality sequence stop: 637.
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 /note="Organ: prostate; Vector: pOTB7; Site_1: XhoI;
 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

FEATURES
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 /organism="Homo sapiens"
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 Site_2: EcoRI; cDNA made by oligo-dT priming.
 Directionally cloned into EcoRI/XhoI sites using the
 following 5' adaptor: GGCACGAG(G). Library constructed by
 Ling Hong in the laboratory of Gerald M. Rubin (University
 of California, Berkeley) using ZAP-cDNA synthesis kit
 (Stratagene) and Superscript II RT (Life Technologies).
 Note: this is a NIH_MGC Library."

ORIGIN
 Query Match 51.7%; Score 620; DB 5; Length 638;
 Best Local Similarity 100.0%; Pred. No. 1e-140;
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 1 GGAACCTAAAAAGAACCTTTATTATTGAGGCAAGGGATGCAACCAATACAAAAATCAA 60
 620 GGAACCTAAAAAGAACCTTTATTATTGAGGCAAGGGATGCAACCAATACAAAAATCAA 561
 61 AAGCTTATCTGGTATTTAACTTTCTTCTCTGCTGTGCAATGAGAGTTAGATTTATT 120
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 VERSION
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 EST.
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 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 898)
 NTH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 AUTHORS
 TITLE
 COMMENT
 Contact: Robert Strausberg, Ph.D.
 Email: cgapbs-remail.nih.gov
 Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
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 High quality sequence stop: 625.
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 /note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
 Average insert size 2.1 Kb."

FEATURES
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 /organism="Homo sapiens"
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 Average insert size 2.1 Kb."

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